

From: Minnifield, Nita  
Sent: Thursday, June 09, 2005 11:36 AM  
To: STIC-Biotech/ChemLib  
Subject: sequence search

CRFE

STIC

09/970076

Please do a commercial and interference sequence search on the following sequences of the above application.

Please search sequences against aa and nt databases.

SEQ ID NO: 1, nt 104-1207 of SEQ ID NO: 1 - 1414 NP

SEQ ID NO: 2, aa 27-321 of SEQ ID NO: 2 - 308 AA  
aa 28-320 of SEQ ID NO: 2  
aa 41-227 of SEQ ID NO: 2  
aa 44-216 of SEQ ID NO: 2  
aa 42-222 of SEQ ID NO: 2

Please provide a paper copy of all results.

Thanks,  
Minnifield  
71976  
Art Unit 1645  
Office REM-3C01  
Mailbox REM-3C18  
571-272-0860

## STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

## Type of Search

NA#: \_\_\_\_\_ AA#: \_\_\_\_\_  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

## Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIS: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

Date completed: \_\_\_\_\_

Searcher: Beverly e 2528

Terminal time: \_\_\_\_\_

Elapsed time: \_\_\_\_\_

CPU time: \_\_\_\_\_

Total time: \_\_\_\_\_

Number of Searches: \_\_\_\_\_

Number of Databases: \_\_\_\_\_

## Search Site

\_\_\_\_\_ STIC

\_\_\_\_\_ CM-1

\_\_\_\_\_ Pre-S

## Type of Search

\_\_\_\_\_ N.A. Sequence

\_\_\_\_\_ A.A. Sequence

\_\_\_\_\_ Structure

\_\_\_\_\_ Bibliographic

## Vendors

\_\_\_\_\_ IG

\_\_\_\_\_ STN

\_\_\_\_\_ Dialog

\_\_\_\_\_ APS

\_\_\_\_\_ Geninfo

\_\_\_\_\_ SDC

\_\_\_\_\_ DARC/Questel

\_\_\_\_\_ Other CLN

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GenCore version 5.1.6  
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# OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 22, 2004, 01:18:40 ; Search time 47.4808 Seconds  
(without alignments)  
2547.963 Million cell updates/sec

Title: US-09-970-076-10

Perfect score: 1131  
Sequence: 1 MSFVFSRGTMTKLTEDR.....STSGKQGNHPCLPAPHT 218

## Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

MODEL=frame+ p2n.model -DEV=xlh  
-O=/cgn2\_1/USPTO\_SPOOL/US09970076/runatc\_21062004\_125531\_8763/app\_query.fasta\_1.2140  
-DB=Issued\_Patents\_NA -QFMT=Fastcap -SUFFIX=rxn1 -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blonum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=psco -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09970076 @CGN\_1\_1\_148 @runatc\_21062004\_125531\_8763 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEOBVERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOC  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/2/lna/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/2/lna/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/2/lna/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/2/lna/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/2/lna/ECTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/2/lna/backfillseq1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1131	100.0	1609	4	US-09-620-312D-8 Sequence 8, Appl
2	966	85.4	2459	4	US-09-833-381-998 Sequence 998, App
3	128.5	11.4	3519	1	US-08-286-889-45 Sequence 45, Appl
4	128.5	11.4	3519	1	US-08-485-618-45 Sequence 45, Appl
5	128.5	11.4	3519	1	US-08-362-652-45 Sequence 45, Appl
6	128.5	11.4	3519	1	US-08-605-672-45 Sequence 45, Appl
7	128.5	11.4	3519	2	US-08-482-293A-45 Sequence 45, Appl
8	128.5	11.4	3519	2	US-08-943-363-45 Sequence 45, Appl
9	128.5	11.4	3519	3	US-09-193-043-45 Sequence 45, Appl
10	128.5	11.4	3519	4	US-09-688-307A-45 Sequence 45, Appl
11	128.5	11.4	3519	4	US-09-350-259-45 Sequence 45, Appl
12	128.5	11.4	3803	1	US-08-485-618-52 Sequence 52, Appl

13	128.5	11.4	3803	1	US-08-362-652-52 Sequence 52, Appl
14	128.5	11.4	3803	1	US-08-605-672-52 Sequence 52, Appl
15	128.5	11.4	3803	2	US-08-482-293A-52 Sequence 52, Appl
16	128.5	11.4	3803	2	US-08-943-363-52 Sequence 52, Appl
17	128.5	11.4	3803	3	US-09-193-043-52 Sequence 52, Appl
18	128.5	11.4	3803	4	US-09-688-307A-52 Sequence 52, Appl
19	128.5	11.4	3803	4	US-09-350-259-52 Sequence 52, Appl
20	122	10.8	3528	1	US-08-286-889-36 Sequence 36, Appl
21	122	10.8	3528	1	US-08-485-618-36 Sequence 36, Appl
22	122	10.8	3528	1	US-08-362-652-36 Sequence 36, Appl
23	122	10.8	3528	1	US-08-605-672-36 Sequence 36, Appl
24	122	10.8	3528	2	US-08-482-293A-36 Sequence 36, Appl
25	122	10.8	3528	2	US-08-943-363-36 Sequence 36, Appl
26	122	10.8	3528	3	US-09-193-043-36 Sequence 36, Appl
27	122	10.8	3528	3	US-09-688-307A-36 Sequence 36, Appl
28	122	10.8	3528	4	US-09-350-259-36 Sequence 36, Appl
29	122	10.8	3597	1	US-08-485-618-54 Sequence 54, Appl
30	122	10.8	3597	1	US-08-362-652-54 Sequence 54, Appl
31	122	10.8	3597	1	US-08-605-672-54 Sequence 54, Appl
32	122	10.8	3597	2	US-08-482-293A-54 Sequence 54, Appl
33	122	10.8	3597	2	US-08-943-363-54 Sequence 54, Appl
34	122	10.8	3597	3	US-09-193-043-54 Sequence 54, Appl
35	122	10.8	3597	4	US-09-688-307A-54 Sequence 54, Appl
36	122	10.8	3597	4	US-09-350-259-54 Sequence 54, Appl
37	114	10.1	2499	1	US-08-485-618-96 Sequence 96, Appl
38	114	10.1	2499	1	US-08-605-672-96 Sequence 96, Appl
39	114	10.1	2499	2	US-08-482-293A-96 Sequence 96, Appl
40	114	10.1	2499	2	US-08-943-363-96 Sequence 96, Appl
41	114	10.1	2499	3	US-09-193-043-96 Sequence 96, Appl
42	114	10.1	2499	3	US-09-688-307A-96 Sequence 96, Appl
43	114	10.1	2499	4	US-09-350-259-96 Sequence 96, Appl
44	114	10.1	3726	1	US-08-173-497-1 Sequence 1, Appl
45	114	10.1	3726	1	US-08-286-889-1 Sequence 1, Appl

## ALIGNMENTS

RESULT 1  
US-09-620-312D-8  
Sequence 8, Application US/09620312D  
Patent No. 6569662  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Asundi, Vinod  
APPLICANT: Zhang, Jie  
APPLICANT: Ren, Feiyun  
APPLICANT: Chen, Rui-hong  
APPLICANT: Zhao, Qing A.  
APPLICANT: Wehman, Tom  
APPLICANT: Xue, Aidiang J.  
APPLICANT: Yang, Yonghong  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Zhou, Ping  
APPLICANT: Ma, Yundong  
APPLICANT: Wang, Duntui  
APPLICANT: Wang, Zhiwei  
APPLICANT: John Tillingshast  
APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
TITLE OF INVENTION: Polypeptides  
FILE REFERENCE: 784C1P2B  
CURRENT APPLICATION NUMBER: US/09/620,312D  
CURRENT FILING DATE: 2000-07-19  
PRIOR APPLICATION NUMBER: 09/552,317  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 09/488,725  
PRIOR FILING DATE: 2000-01-21  
NUMBER OF SEQ ID NOS: 1105  
SOFTWARE: pc\_fl\_genes Version 1.0  
SEQ ID NO 8  
LENGTH: 1609  
TYPE: DNA

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/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (309)..(1202)
US-09-620-312D-8

Alignment Scores:
Pred. No.:      8e-148      Length:      1609
Score:          1131.00     Matches:      218
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     100.00%     Indels:      0
DB:              4          Gaps:         0

US-09-970-076-10 (1-218) x US-09-620-312D-8 (1-1609)

QY      1 MetSerPheIleValPheSerThrArgGlyThrThrLeuMetIysLeuThrGluAspArg 20
Db      546 ATGTCCTTATTTGTTTCTCCACCCGAGGAACACCTTAATGAAACTGACGAAGACAGA 605

QY      21 GluGlnIleArgGlnGlyLeuGlnGluLeuGlnIysValLeuProGlyGlyAspThrTyr 40
Db      606 GAACAAATCCGTCAGAGCCTAGAAAGACTCCAGAAAGTTCTGCCAGAGAGACACTTAC 665

QY      41 MetHisGlnGlyPheGluArgAlaSerGlnGlnIleTyrTyrGluAsnArgGlnGlyTyr 60
Db      666 ATGCATGAAGATTGAAAGGGCCAGTGACGAGATTATTATGAAACAGACAAAGGATAC 725

QY      61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGlyLeuHisGluAspLeuPhePhe 80
Db      726 AGGACAGCCAGCGTCATCTGCTTGTGACTGATGAGAACTCCAGAAAGATCTCTTTTTC 785

QY      81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyValIleValTyrCysValGly 100
Db      786 TATTCAGAGAGGAGGAGCTAATAGCTCTGAGATCTTGTCGATTTGTTACTGTGTGCT 845

QY      101 ValIysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhe 120
Db      846 GTGAAAGATTCAATGAGACACAGCTGGCCGGATTGGGACAGTAAGATCATGTGTTT 905

QY      121 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSer 140
Db      906 CCCGTAATGACGGCTTTCAGGCTCTGCAGGACATCACTCAATTTTGAAGAGGCC 965

QY      141 CysIleGlnIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 160
Db      966 TGCATCGAAATTTCTAGACGCTGAAACCATCCACATATGTGACGAGAGTCAATTCAGTT 1025

QY      161 ValValaArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPhe 180
Db      1026 GTCGTGAGAGGAAACGGCTTCGACATGCCGCAACGTGACAGGGTCTCTGCAAGCTTC 1085

QY      181 LysIleAsnAspSerValThrLeuSerLysSerLeuGlnSerProTTPValSerSerThr 200
Db      1086 AAGATCAATGACTCGCTCAGACTCAGTAAGTCTTGACAGAGTCCATGGGTTTCTTCGCA 1145

QY      201 SerGlyPheLysGluGlyAsnSerHisProCysLeuProAlaArgProHisThr 218
Db      1146 AGTGCCTTCAGAGGAAAGGAAATTCACCCCTTGTCTTCACGAGAGGCCACACACA 1199

RESULT 2
US-09-833-381-998
/ Sequence 998, Application US/09833381
/ Patent No. 6672186
/ GENERAL INFORMATION:
/ APPLICANT: Robison, Keith E.
/ TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
/ FILE REFERENCE: 5800-119
/ CURRENT APPLICATION NUMBER: US/09/833,381
/ PRIOR FILING DATE: 2001-04-11
/ PRIOR APPLICATION NUMBER: 09/516,448
/ NUMBER OF SEQ ID NOS: 2050
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/ SOFTWARE: FASTSEQ for Windows Version 3.0
/ SEQ ID NO 998
/ LENGTH: 2459
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(2459)
/ OTHER INFORMATION: n = A,T,C or G
US-09-833-381-998

Alignment Scores:
Pred. No.:      2.01e-124      Length:      2459
Score:          966.00     Matches:      188
Percent Similarity: 100.00%   Conservative: 2
Best Local Similarity: 98.95% Mismatches: 0
Query Match:     85.41%     Indels:      0
DB:              4          Gaps:         0

US-09-970-076-10 (1-218) x US-09-833-381-998 (1-2459)

QY      1 MetSerPheIleValPheSerThrArgGlyThrThrLeuMetIysLeuThrGluAspArg 20
Db      649 ATGTCCTTATTTGTTTCTCCACCCGAGGAACAACTTAATGAAACTGACGAAGACAGA 708

QY      21 GluGlnIleArgGlnGlyLeuGlnGluLeuGlnIysValLeuProGlyGlyAspThrTyr 40
Db      709 GAACAAATCCGTCAGAGCCTAGAAAGACTCCAGAAAGTTCTGCCAGAGAGACACTTAC 768

QY      41 MetHisGlnGlyPheGluArgAlaSerGlnGlnIleTyrTyrGluAsnArgGlnGlyTyr 60
Db      769 ATGCATGAAGATTGAAAGGGCCAGTGACGAGATTATTATGAAACAGACAAAGGCTAC 828

QY      61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGlyLeuHisGluAspLeuPhePhe 80
Db      829 AGGACAGCCAGCGTCATCTGCTTGTGACTGATGAGAACTCCATGAAAGATCTCTTTTTC 888

QY      81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyValIleValTyrCysValGly 100
Db      889 TATTCAGAGAGGAGGAGCTAATAGCTCTGAGATCTTGTCGATTTGTTACTGTGTGCT 948

QY      101 ValIysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhe 120
Db      949 GTGAAAGATTCAATGAGACACAGCTGGCCGGATTGCGGACGTAAAGATCATGTGTTT 1008

QY      121 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSer 140
Db      1009 CCCGTAATGACGGCTTTCAGGCTCTGCAGGACATCACTCAATTTTGAAGAGTCC 1068

QY      141 CysIleGlnIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 160
Db      1069 TGCATCGAAATTTCTAGACGCTGAAACCATCCACATATGTGACGAGAGTCAATTCAGTT 1128

QY      161 ValValaArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPhe 180
Db      1129 GTCGTGAGAGGAAACGGCTTCGACATGCCGCAACGTGACAGGGTCTCTGCAAGCTTC 1188

QY      181 LysIleAsnAspSerValThrLeuSerLys 190
Db      1189 AAGATCAATGACTCGTGCACATCAATGAG 1218

RESULT 3
US-08-286-889-45
/ Sequence 45, Application US/08286889
/ Patent No. 5470953
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Mich
/ TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 51
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Garstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Sear Tower
```



CITY: Chicago  
 STATE: Illinois  
 COUNTRY: United States  
 ZIP: 60606-6402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/286,889  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/173,497  
 FILING DATE: 23-DEC-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Williams Jr., Joseph A.  
 REGISTRATION NUMBER: P38,659  
 REFERENCE/DOCKET NUMBER: 27866/32168  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312-474-6300  
 TELEFAX: 312-474-0448  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 45:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3519 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 52..3519  
 US-08-286-889-45

Alignment Scores:		
Pred. No.:	5.9e-07	3515
Score:	128.50	Matches: 50
Percent Similarity:	46.82	Conservative: 31
Best local Similarity:	28.904	Mismatches: 69
Query Match:	11.364	Indels: 23
DB:	1	Gaps: 9

[illegible]

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Oy      142  1leglufieulalaaagluPProserPhrllleCysalalylgluSePhelGlnvalval 161
          :::::
Db      1051  -----ATCTTGGCATTTAGAGAACCGAATCAAGGTCAAAATGATCTTTTCAGCAGCAG 110
          :::::
Oy      162  ValArgGlyaenGlyPheNArgHisAlaArgAsnValaAp 174
          :::::
Db      1105  ATGTGCACAGAGGTTTACGCTCAAGCTCTTCAATAGAT 1143
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RESULT 4  
US-08-485-618-45  
08-08-2008 14:00:00

```

; sequence 45, Application US/08485818
; Patent No. 5728533
; GENERAL INFORMATION:

```

GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
APPLICANT: Van der Vieren, Monica

TITLE OF INVENTION:	No. 5728533e1 Human	2 Integrin Alpha Subunit
NUMBER OF SEQUENCES:	103	

1 CORRESPONDENCE ADDRESS:  
1  
1 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 Sou  
CITY: Chicago

STATE: Illinois  
COUNTRY: United States  
RD: 0000000000

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; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY

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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/485,618  
FILING DATE:

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;

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APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIORITY APPLICATION DATA:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,885  
FILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652

FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:

;; NAME: Williams Jr., Joseph A.  
; REGISTRATION NUMBER: 38,659  
;

```

; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION
;

```

TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448

TELE: 25-3856  
INFORMATION FOR SEQ ID NO:  
SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:  
LENGTH: 3519 base pairs  
TYPE: nucleic acid

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STRANDEDNESS: single
;
TOPOLOGY: linear
```

```

; MOLECULE TYPE: CDNA
; FEATURE:
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```

```

; NAME/KEY: CDS
; LOCATION: 52..3519
;

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US-08-485-618-45

Alignment scores:  
Pred. No.: 5.9e-07  
Score: 128.50

Percent Similarity: 46.82%  
Best Local Similarity: 28.90%

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Query Match: 11.36%
DB: 1
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US-09-970-076-10 (1-218) x US-08-485-618-45 (1-3519)

Alignment scores:	
Pred. No.:	5,9e-07
Score:	18.50
Percent Similarity:	46.82%
Best Local Similarity:	28.90%
Query Match:	11.36%
DB:	1
Length:	3515
Matches:	50
Conservative:	31
Mismatches:	69
Indels:	23
Gaps:	9

US-09-970-076-10 (1-218) x US-08-485-618-45 (1-3519)

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 Db 664 ACGGAATTCAAGAGAGAGCTGAGCCCTCAGAGCCTGGTGGATGCATGCTCCAGCTCAA 723  
 QY 32 LysValLeuProGlyGlyAspThrTyrMetHisgluGlyPhegluAglAsaSerGln 51  
 Db 724 -----GGCCTGACGACACAGCCTCGGGCATCCGAAAGTGGTGAAGAG 768  
 QY 52 IleTyrTyrGluAsnArgGlnGlyTyrArgThrAla---SerValIleIleAlaLeuThr 70  
 Db 769 CTATTTCATACCAAGATGGGGCCGAAAGAGTCCCAAGAAATATCTAATTGTCTACACA 828  
 QY 71 AspGlyGluLeuHisgluAspLeuPhePheTyrSerGlu-----ArgGluAlaAsnArg 88  
 Db 829 GATGGCGAAGAAATTCAGAGACCCCTCGAGATATGACATGTCATCCCGAAGCAGAGAAA 888  
 QY 89 SerArgAspLeuGlyAlaIleValTyrCysValGlyValLysAsp---PheAsnGlu--- 106  
 Db 889 GCT-----GGGATCATTCGCTATCTATAGGGGTGGAGATGCTCCGGGAAACC 939  
 QY 107 ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhePro 121  
 Db 940 ACTGCCCTTACAGAGACTCAACACCATTTGGCTCAGCTCCCTCGCAGACCATGTTTCAAG 999  
 QY 122 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 141  
 Db 1000 GTGGGCAAT---TTTGTAGCACTTCGACATCCAGCGCAAAATTCAGAGAAA----- 1050  
 QY 142 IleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyLysSerPheGlnVal 161  
 Db 1051 -----ATCTTGTGCATTGAAGAACCGAATCAAGTCAAGTAGTTCTTTCACAGACGAG 1104  
 QY 162 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 174  
 Db 1105 ATGTCAACAAGAGTTTTCAGCTCAGCTCTCTCAATGAT 1143  
 RESULT 5  
 US-08-362-652-45  
 ; Sequence 45, Application US/08362652  
 ; Patent No. 5766850  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gallatin, W. Michael  
 ; TITLE OF INVENTION: Van der Vlieten, Monica  
 ; NUMBER OF SEQUENCES: 93  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 ; STREET: 233 South Wacker Drive, 6300 Sear Tower  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: United States  
 ; ZIP: 60606-6402  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: IBM PC compatible  
 ; SOFTWARE: Patent Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/362,652  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/173,497  
 ; FILING DATE: 23-DEC-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/286,889  
 ; FILING DATE: 5-AUG-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Williams Jr., Joseph A.  
 ; REGISTRATION NUMBER: 38,659  
 ; REFERENCE/DOCKET NUMBER: 27866/32391  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312-474-6300

; TELEFAX: 312-474-0448  
 ; TELEX: 25-3856  
 ; INFORMATION FOR SEQ ID NO: 45:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 3519 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 52..3519  
 ; US-08-362-652-45  
 Alignment Scores:  
 Pred. No.: 5,9e-07 Length: 3519  
 Score: 128.50 Matches: 50  
 Percent Similarity: 46.82% Conservative: 31  
 Best Local Similarity: 28.90% Mismatches: 69  
 Query Match: 11.36% Indels: 23  
 Gaps: 9  
 US-09-970-076-10 (1-218) x US-08-362-652-45 (1-3519)  
 QY 12 ThrluWcltYlsuThrgluAspArglInglleArgInglYleuGlulLeuGln 31  
 Db 664 ACGGAATTCAAGAGAGAGCTGAGCCCTCAGAGCCTGGTGGATGCATGCTCCAGCTCAA 723  
 QY 32 LysValLeuProGlyGlyAspThrTyrMetHisgluGlyPhegluAglAsaSerGln 51  
 Db 724 -----GGCCTGACGACACAGCCTCGGGCATCCGAAAGTGGTGAAGAG 768  
 QY 52 IleTyrTyrGluAsnArgGlnGlyTyrArgThrAla---SerValIleIleAlaLeuThr 70  
 Db 769 CTATTTCATACCAAGATGGGGCCGAAAGAGTCCCAAGAAATATCTAATTGTCTACACA 828  
 QY 71 AspGlyGluLeuHisgluAspLeuPhePheTyrSerGlu-----ArgGluAlaAsnArg 88  
 Db 829 GATGGCGAAGAAATTCAGAGACCCCTCGAGATATGACATGTCATCCCGAAGCAGAGAAA 888  
 QY 89 SerArgAspLeuGlyAlaIleValTyrCysValGlyValLysAsp---PheAsnGlu--- 106  
 Db 889 GCT-----GGGATCATTCGCTATCTATAGGGGTGGAGATGCTCCGGGAAACC 939  
 QY 107 ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhePro 121  
 Db 940 ACTGCCCTTACAGAGACTCAACACCATTTGGCTCAGCTCCCTCGCAGACCATGTTTCAAG 999  
 QY 122 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 141  
 Db 1000 GTGGGCAAT---TTTGTAGCACTTCGACATCCAGCGCAAAATTCAGAGAAA----- 1050  
 QY 142 IleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyLysSerPheGlnVal 161  
 Db 1051 -----ATCTTGTGCATTGAAGAACCGAATCAAGTCAAGTAGTTCTTTCACAGACGAG 1104  
 QY 162 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 174  
 Db 1105 ATGTCAACAAGAGTTTTCAGCTCAGCTCTCTCAATGAT 1143  
 RESULT 6  
 US-08-605-672-45  
 ; Sequence 45, Application US/08605672  
 ; Patent No. 5817515  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gallatin, W. Michael  
 ; TITLE OF INVENTION: Van der Vlieten, Monica  
 ; NUMBER OF SEQUENCES: 103  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 ; STREET: 233 South Wacker Drive, 6300 Sear Tower  
 ; CITY: Chicago

STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/605,672  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3519 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 52..3519  
US-08-605-672-45

Alignment Scores:  
Pred. No.: 5,9e-07 Length: 3519  
Score: 128.50 Matches: 50  
Percent Similarity: 46.82% Conservative: 31  
Best Local Similarity: 28.90% Mismatches: 69  
Query Match: 11.36% Indels: 23  
DB: 1 Gaps: 9

US-09-970-076-10 (1-218) x US-08-605-672-45 (1-3519)

Qy 12 ThrleuMetLysLeuThrGluValArgGluGlnIleArgGlnIleLeuGlnIleLeuGln 31  
Db 664 ACGGAATTCAG 723  
Qy 32 LysValLeuProGlyGlyAspThrGlyMetHisGluGlyPheGluArgLysSerGlu 51  
Db 724 -----GGCCTGAGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 768  
Qy 52 IleTyrGluAsnArgGlnIleGlyArgThrAla-----SerValIleGleAlaLeuThr 70  
Db 769 CTAATTCATAG 828  
Qy 71 ArgGlyGluLeuHisGluAspLeuPhePheTyrSerGlu-----ArgGluAlaAsnArg 88  
Db 829 GATGGGCAAGATTCAG 888  
Qy 89 SerArgAspLeuGlyAlaIleValIleTyrCysValGlyValLysAsp-----PheAsnGlu 106  
Db 889 GCT-----GGGATCATTCGCTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 939  
Qy 107 ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhePro 121

Db 940 ACTGCCCTACAG 999  
Qy 122 ValAsnArgGlyPheGlnAlaLeuGlnIleIleHisSerIleLeuLysSerCys 141  
Db 1000 GTGGGCAAT-----TTGTAGACATTCGAGCATTCAGAGAGAGAGAGAGAGAGAGAG 1050  
Qy 142 IleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 161  
Db 1051 -----ATCTTGGCATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1104  
Qy 162 ValArgGlyAsnGlyPheArgHisAlaArgHisValAsp 174  
Db 1105 ATGTCAAG 1143

RESULT 7  
US-08-482-293A-45  
Sequence 45, Application US/08482293A  
Patent No. 5831029  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
TITLE OF INVENTION: No. 5831029e1 Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum  
STREET: 233 South Wacker Drive, 6300 Seear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,293A  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3519 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 52..3519  
US-08-482-293A-45

Alignment Scores:  
Pred. No.: 5,9e-07 Length: 3519  
Score: 128.50 Matches: 50  
Percent Similarity: 46.82% Conservative: 31  
Best Local Similarity: 28.90% Mismatches: 69

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Query Match:      11.36%      Indels:      23
DB:               2          Gaps:         9

US-09-970-076-10 (1-218) x US-08-482-293A-45 (1-3519)

Qy      12  ThrleuMetIyLeuThrgluAerArgIuGlInleArgInglyLeuGlInleuGlIn 31
      Db      664  ACGGAATTCAAGAGAGCCCTGAGCCCTGAGCCCTGAGATGCATGCTCAGCTCCAA 723
Qy      32  LysValIleuProGlyIyAerThrTyMetIleGlIyPhegluAerAlaSerGlIn 51
      Db      724  -----GGCTGACGTACAGACCCCTGAGATGACATCCGAAAGTGCTGAAGAG 768
Qy      52  IleTyTyrgluAerArgInglyTyArgThrAla---SerValIleIleAlaIleuThr 70
      Db      769  CATTTCATACAGAAATGGGGCCCGAAAGTGCCAGAAAGATACATATTGTCATCA 828
Qy      71  AserGlyIleuHleGlAerleuPhePheTySerGlu-----ArgIuAlaAerArg 88
      Db      829  GATGGCGCAAAATTCAGAGACCCCTGAGATGACATGTCATCCCTGAAGCAGAGAA 888
Qy      89  SerArgAerleuGlyAlaIleValTyrcyValIyValyAer---PheAerGlu--- 106
      Db      889  GCT-----GGGATCATTCGCTATGCTATAGGGGTGGAGATGCTTCGGGAACCC 939
Qy      107  ThrGluAerAlaArgIle-----AlaAerSerTyAerPheIleValPhePro 121
      Db      940  ACTGCCCTACAGAGAGTGAACCATGCTGCTCAGCTCCCTGACAGACCATGTTCAAG 999
Qy      122  ValAerAerGlyPheGlAlaIleuGlInglyIleIleHleAerIleuTyLeuTySerCy 141
      Db      1000  GTGGGCAT---TTTGTAGCATTCGACAGCATCCAGCGCAAAATTCAGAGAA--- 1050
Qy      142  IleGluIleuAlaIleGlIyProSerThrIleCyValIyGluSerPheGlIleVal 161
      Db      1051  -----ATCTTGCCATTGAAGAACCAATCAAGTCAAGTATGTTCTTTCAGACAG 1104
Qy      162  ValArgGlyAerGlyPheArgHleAlaArgAerValAer 174
      Db      1105  ATGTCAAGAAAGTTTCAGCTCAGCTCTCATATGAT 1143

RESULT 8
US-08-943-363-45
/ Sequence 45, Application US/08943363
/ Patent No. 5837478
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 114
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Seear Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/943.363
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ PRIOR APPLICATION DATA:

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/ APPLICATION NUMBER: US 08/362,652
/ FILING DATE: 21-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32684
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ. ID NO.: 45:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3519 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 52..3519
/ US-08-943-363-45

Alignment Scores:
Pred. No.: 5.9e-07 Length: 3519
Score: 128.50 Matches: 50
Percent Similarity: 46.82% Conservative: 31
Best Local Similarity: 28.90% Mismatches: 69
Query Match: 11.36% Indels: 23
DB: Gaps: 9

US-09-970-076-10 (1-218) x US-08-943-363-45 (1-3519)

Qy      12  ThrleuMetIyLeuThrgluAerArgIuGlInleArgInglyLeuGlInleuGlIn 31
      Db      664  ACGGAATTCAAGAGAGCCCTGAGCCCTGAGCCCTGAGATGCATGCTCAGCTCCAA 723
Qy      32  LysValIleuProGlyIyAerThrTyMetIleGlIyPhegluAerAlaSerGlIn 51
      Db      724  -----GGCTGACGTACAGACCCCTGAGATGACATCCGAAAGTGCTGAAGAG 768
Qy      52  IleTyTyrgluAerArgInglyTyArgThrAla---SerValIleIleAlaIleuThr 70
      Db      769  CATTTCATACAGAAATGGGGCCCGAAAGTGCCAGAAAGATACATATTGTCATCA 828
Qy      71  AserGlyIleuHleGlAerleuPhePheTySerGlu-----ArgIuAlaAerArg 88
      Db      829  GATGGCGCAAAATTCAGAGACCCCTGAGATGACATGTCATCCCTGAAGCAGAGAA 888
Qy      89  SerArgAerleuGlyAlaIleValTyrcyValIyValyAer---PheAerGlu--- 106
      Db      889  GCT-----GGGATCATTCGCTATGCTATAGGGGTGGAGATGCTTCGGGAACCC 939
Qy      107  ThrGluIleuAlaArgIle-----AlaAerSerTyAerPheIleValPhePro 121
      Db      940  ACTGCCCTACAGAGAGTGAACCATGCTGCTCAGCTCCCTGACAGACCATGTTCAAG 999
Qy      122  ValAerAerGlyPheGlAlaIleuGlInglyIleIleHleAerIleuTyLeuTySerCy 141
      Db      1000  GTGGGCAT---TTTGTAGCATTCGACAGCATCCAGCGCAAAATTCAGAGAA--- 1050
Qy      142  IleGluIleuAlaIleGlIyProSerThrIleCyValIyGluSerPheGlIleVal 161
      Db      1051  -----ATCTTGCCATTGAAGAACCAATCAAGTCAAGTATGTTCTTTCAGACAG 1104
Qy      162  ValArgGlyAerGlyPheArgHleAlaArgAerValAer 174
      Db      1105  ATGTCAAGAAAGTTTCAGCTCAGCTCTCATATGAT 1143

RESULT 9
US-09-193-043-45
/ Sequence 45, Application US/09193043
/ Patent No. 6251395
/ GENERAL INFORMATION:

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; APPLICANT: Gallatin, Michael W.
; TITLE OF INVENTION: No. 6251395el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/193.043
; CURRENT FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 45
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(3516)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-193-043-45

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Alignment Scores:
Pred. No.: 5.9e-07 Length: 3519
Score: 128.50 Matches: 50
Percent Similarity: 46.82% Conservative: 31
Best Local Similarity: 28.90% Mismatches: 69
Query Match: 11.36% Indels: 23
DB: Gaps: 9

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US-09-970-076-10 (1-218) x US-09-193-043-45 (1-3519)

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QY 12 ThrleuMeTlyLeuThngluAaPrgluGlnlleaGnglyLeuGluGluGln 31
DB 664 ACGGAATTCAAGACAGCGCTGAGCCCTGAGCGCTGGTGATGCCATGCTCCAG 723
QY 32 LysValLeuProGlyAaPrgThTyTmeChlsGluGlyPheGluAraLseGluGln 51
DB 724 -----GGCTGACGTACACAGCGCTGGGATCCAGAAAGTGTTGAAGAG 768
QY 52 IleTyTyGluAaPrgGlnGlyTyTArGThraLa--SerValIlelleAaLeuThr 70
DB 769 CTAATTCATACAGAAATGGGGCCGGAAGAGTCAAGATCTAATGTCATCACA 828
QY 71 AaPrgGlyLeuAaPrgLeuAaPrgLeuAaPrgLeuAaPrgLeuAaPrgLeuAaPrg 88
DB 829 GATGGGCAAGAAATTCAGAGACCCCTGAGATATACATGTCATCCCTGAAGCAGAAA 888
QY 89 SerArgAaPrgLeuGlyAaPrgLeuAaPrgLeuAaPrgLeuAaPrgLeuAaPrgLeu 106
DB 889 GCT-----GGATCATTCGCTATGCTATGAGGGGTGGAGATCCCTCCGGGAAACC 939
QY 107 ThrGlnLeuAaPrgIle-----AaAaPrgSerLyAaPrgIleValPhePro 121
DB 940 ACTGCCCTACAGAGACTGAACACATGGCTCAGCTCCCTCGCAGAGACAGGTTCAG 999
QY 122 ValAaAaPrgGlyPheGlnAaPrgLeuGlnGlyIlelleAaPrgLeuAaPrgLeuAaPrg 141
DB 1000 GTGGGCAAT--TTTGTAGCACTTCGAGCATCCAGCGCAAAATTCAGAGAAA----- 1050
QY 142 IleGluIleLeuAaPrgIleValPheProSerThryIleCyAaGlyGluSerPheGlnVal 161
DB 1051 -----ATCTTGCCATTCAGAAAGCAATCAAGCTCAAGTAGTTCCTTTTACAGACAG 1104
QY 162 ValAaPrgGlyAaPrgGlyPheAaPrgIleValAaPrgAaPrgValAaPrg 174
DB 1105 ATGTCAAGAAAGGTTTCAGCTCAGCTCTCTCAATGAT 1143

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RESULT 10
US-09-688-307A-45
; Sequence 45, Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; TITLE OF INVENTION: No. 6432404el Human Beta-2
; FILE REFERENCE: 27866/36646
; CURRENT APPLICATION NUMBER: US/09/688,307A
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605,672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 45
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(3516)
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-688-307A-45

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Alignment Scores:
Pred. No.: 5.9e-07 Length: 3519
Score: 128.50 Matches: 50
Percent Similarity: 46.82% Conservative: 31
Best Local Similarity: 28.90% Mismatches: 69
Query Match: 11.36% Indels: 23
DB: Gaps: 9

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US-09-970-076-10 (1-218) x US-09-688-307A-45 (1-3519)

```

QY 12 ThrleuMeTlyLeuThngluAaPrgluGlnlleaGnglyLeuGluGluGln 31
DB 664 ACGGAATTCAAGACAGCGCTGAGCCCTGAGCGCTGGTGATGCCATGCTCCAG 723
QY 32 LysValLeuProGlyAaPrgThTyTmeChlsGluGlyPheGluAraLseGluGln 51
DB 724 -----GGCTGACGTACACAGCGCTGGGATCCAGAAAGTGTTGAAGAG 768
QY 52 IleTyTyGluAaPrgGlnGlyTyTArGThraLa--SerValIlelleAaLeuThr 70
DB 769 CTAATTCATACAGAAATGGGGCCGGAAGAGTCAAGATCTAATGTCATCACA 828
QY 71 AaPrgGlyLeuAaPrgLeuAaPrgLeuAaPrgLeuAaPrgLeuAaPrgLeuAaPrg 88
DB 829 GATGGGCAAGAAATTCAGAGACCCCTGAGATATACATGTCATCCCTGAAGCAGAAA 888
QY 89 SerArgAaPrgLeuGlyAaPrgLeuAaPrgLeuAaPrgLeuAaPrgLeuAaPrgLeu 106
DB 889 GCT-----GGATCATTCGCTATGCTATGAGGGGTGGAGATCCCTCCGGGAAACC 939
QY 107 ThrGlnLeuAaPrgIle-----AaAaPrgSerLyAaPrgIleValPhePro 121
DB 940 ACTGCCCTACAGAGACTGAACACATGGCTCAGCTCCCTCGCAGAGACAGGTTCAG 999
QY 122 ValAaAaPrgGlyPheGlnAaPrgLeuGlnGlyIlelleAaPrgLeuAaPrgLeuAaPrg 141
DB 1000 GTGGGCAAT--TTTGTAGCACTTCGAGCATCCAGCGCAAAATTCAGAGAAA----- 1050

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[illegible]

Accession	Sequence	Length
Db 940	ACTGCCCTACAGAGAGCTGACACCATTTGGCTCAGCTCCCTCGCAGAGACCAAGTGTCAAG	999
Qy 122	Valaenapgilypheglalaleuglnclyllellelserllleulylserys	141
Db 1000	GTGGGCAAT---TTTGAGCACTTCGCAGCATCCAGCGCAAAATTCAGAGAA-----	1055
Qy 142	llegullleulalalagluPproserthrilecysalaglgluserpheglvalal	161
Db 1051	-----ATCTTGGCCATTGAAGAAGCAATCAAGGTCAAGTAGTCTCTTCAGACGAG	1104
Qy 162	ValargliyaengilyphearghiealargasenValaep	174
Db 1105	ATGTCAAGAAAGGTTTCAGCTCAGCTCTCATGAT	1143
RESULT 12		
US-08-485-618-52		
Sequence 52, Application US/08485618		
Patent No. 5728533		
GENERAL INFORMATION:		
APPLICANT: Gallatin, W. Michael		
APPLICANT: Van der Vlieten, Monica		
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit		
NUMBER OF SEQUENCES: 103		
CORRESPONDENCE ADDRESS:		
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun		
STREET: 233 South Wacker Drive, 6300 Sear Tower		
CITY: Chicago		
STATE: Illinois		
COUNTRY: United States		
ZIP: 60606-6402		
COMPUTER READABLE FORM:		
MEDIUM TYPE: Floppy disk		
COMPUTER: IBM PC compatible		
OPERATING SYSTEM: PC-DOS/MS-DOS		
SOFTWARE: Patentn Release #1.0, Version #1.25		
CURRENT APPLICATION DATA:		
APPLICATION NUMBER: US/08/485,618		
FILING DATE:		
CLASSIFICATION: 435		
PRIOR APPLICATION DATA:		
APPLICATION NUMBER: US 08/173,497		
FILING DATE: 23-DEC-1993		
PRIOR APPLICATION DATA:		
APPLICATION NUMBER: US 08/286,889		
FILING DATE: 5-AUG-1994		
PRIOR APPLICATION DATA:		
APPLICATION NUMBER: US 08/362,652		
FILING DATE: 21-DEC-1994		
ATTORNEY/AGENT INFORMATION:		
NAME: Williams Jr., Joseph A.		
REGISTRATION NUMBER: 38,659		
REFERENCE/DOCKET NUMBER: 27866/32797		
TELECOMMUNICATION INFORMATION:		
TELEPHONE: 312-474-6300		
TELEFAX: 312-474-0448		
TELEX: 25-3856		
INFORMATION FOR SEQ ID NO: 52:		
SEQUENCE CHARACTERISTICS:		
LENGTH: 3803 base pairs		
TYPE: nucleic acid		
STRANDEDNESS: single		
TOPOLOGY: linear		
MOLECULE TYPE: CDNA		
FEATURE:		
NAME/KEY: CDS		
LOCATION: 1..3486		
US-08-485-618-52		
Alignment Scores:		
Pred. No.: 6.72e-07	Length: 3803	
Score: 128.50	Matches: 50	
Percent Similarity: 46.82%	Conservative: 31	

```

: ATORNEY/AGENT INFORMATION:
: NAME: William Jr., Joseph A.
: REGISTRATION NUMBER: 38,659
: REFERENCE/DOCKET NUMBER: 27866/32391
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-474-6300
: TELEFAX: 312-474-0448
: TELEX: 25-3866
: INFORMATION FOR SEQ ID NO: 52:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3803 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..3486
: US-08-362-652-52

Alignment Scores:
Pred. No.: 6.72e-07 Length: 3803
Score: 128.50 Matches: 50
Percent Similarity: 46.82% Conservative: 31
Best Local Similarity: 28.90% Mismatch: 69
Query Match: 11.36% Indels: 23
Gaps: 9

US-09-970-076-10 (1-218) x US-08-362-652-52 (1-3803)

QY 12 ThrleuwtclyleThrluaspArglGlnlleatrglnglyLeuaglululeGln 31
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 613 ACGGAATTCAAAGAGACGCTGAGCCCTCAGAGCCCTGGATGCCATGTCAGCTCCAA 672

QY 32 LysValleuProGlyGlyAspThrTyrMetHisGluGlyPheGluArgAlaSerGlu 51
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 673 -----GacCTGACGTTACACAGCCCTCGGCGATCCAGAAAGTGCTGAAGAG 717

QY 52 lIeTyrGluAenArgGlnGlyTyrArgThrAla---SerValIleAlaLeuThr 70
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 718 CTATTTCATTACCAAGAAATGGGGCCCGAAGTGCACAGAAATCTAATGTCTATCACA 777

QY 71 AspGlyGluLeuHisGluAspLeuPhePheTyrSerGlu-----ArgGluAlaAsnArg 88
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 778 GATGGGGCAGAAATTCAGAGACCCCTGGAGTATAGACATGTCATCCTCGAAGCAGAGAAA 837

QY 89 SerArgAspLeuGlyAlaIleValTyrCysValGlyValLysAsp---PheAsnGlu--- 106
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 838 GCT-----GGATCATTCGCTGATGCTAATGGGGGAGGAGATGCTTCGGAGACC 888

QY 107 ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhePro 121
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 889 ACTGCCCTACAGAGACTGAACAACCATTTGGCTCAGCTCCCTCGCAGACACAGTGTCAAG 948

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QY 142 lIeGluIleLeuAlaIlaGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 161
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QY 162 ValArgGlyAsnGlyPheArgHisAlaIArgAsnValaAsp 174
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RESULT 14
US-08-605-672-52
: Sequence 52, Application US/08605672
: Patent No. 5817515
: GENERAL INFORMATION:
: APPLICANT: Gallatin, W. Michael
: APPLICANT: Van der Vieren, Monica

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TITLE OF INVENTION: No. 5817515e1 Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Sear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/605,672  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
FILING DATE: 25-3856  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3803 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..3486  
US-08-605-672-52  
US-09-970-076-10 (1-218) x US-08-605-672-52 (1-3803)  
Alignment Scores:  
Pred. No.: 6,72e-07 Length: 3803  
Score: 128.50 Matches: 50  
Percent Similarity: 46.82% Conservative: 31  
Best Local Similarity: 28.90% Mismatches: 69  
Query Match: 11.36% Indels: 23  
Gaps: 9  
DB: 1  
US-09-970-076-10 (1-218) x US-08-605-672-52 (1-3803)  
12 ThrleuMetlyleuThGlnuAphrglGlnlileagnglyleuGlnuLength 31  
Db 613 ACGGAATTCAGAGAGCGCTGAGCCCTGAGCGCTGATGCGATGCTGCAAGCTCAA 672  
Qy 32 LysValleuProGlyGlyAspThrTyMetHlsGlnuGlyPheGlnuArlsersGlnu 51  
Db 673 -----GGCCTGACGTACACAGCCTCGGCATCCAGAAAGTGTAAGAG 717  
Qy 52 lleyTyTgLuAsnArGlnlYtArGThrala---SerVallellelealeuThr 70  
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Qy 71 AapglYtAluAuhlsGlnuAphrleuPheThyrsGlu-----ArgGluAlaAsnArG 88  
Db 778 GATGGGCAAGAAATTCAGAGACCCCTCGAGTATAGACATGTATCCCTGGAAGCAGAGAA 837

Qy 89 SerArgAspleuGlyAlaIleValTyCySvalGlyValIysAsp---PheAenglu--- 106  
Db 838 GCT-----GGATCATTCGCTATGCTATAGGGGTGGAGATGCTCCGGAAACC 888  
Qy 107 ThGlnleuAlaArgile-----AlaAspSerlyAspHlsValPhePro 121  
Db 889 ACTGCCCTACAGAGCGTGAACACCATTTGCTCAGCTCCCTCGAGACCACTGTTCAAG 948  
Qy 122 ValAsnAspGlyPheGlnAlaIleGlnGlylleIleHlsSerlleuTySlysSerCys 141  
Db 949 GTGGGCAT---TTTGTAGCATCTCCAGCATCCAGCGCAATTCAGAGAA----- 999  
Qy 142 lIeGlnlleuAlaIaGluProSerThrIleCyAlaGlyIuSerPheGlnVal 161  
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Qy 162 ValArgGlyAsnGlyPheArgHlsAlaAsnValAsp 174  
Db 1054 ATGTCAAGAGAGTTTCACTCAGCTCTCTCATGAT 1092  
RESULT 15  
US-08-482-293A-52  
Sequence 52, Application US/08482293A  
Patent No. 5831029  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
APPLICANT: Van der Vliet, Monica  
TITLE OF INVENTION: No. 5831029e1 Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Sear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,293A  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
FILING DATE: 25-3856  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3803 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..3486  
US-08-482-293A-52





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Run on: June 22, 2004, 02:37:46 ; Search time 324.721 Seconds  
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Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database : Published Applications NA:  
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3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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4	966.5	85.5	1608	15	US-10-201-292-35	Sequence 33, Appl1
5	966	85.4	1008	15	US-10-038-307-25	Sequence 25, Appl1
6	966	85.4	1008	15	US-10-201-292-25	Sequence 25, Appl1
7	966	85.4	1047	15	US-10-038-307-21	Sequence 21, Appl1
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9	966	85.4	1056	15	US-10-038-307-23	Sequence 23, Appl1
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15	966	85.4	1650	15	US-10-038-307-9	Sequence 9, Appl1
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19	966	85.4	1650	15	US-10-201-292-13	Sequence 13, Appl1
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21	966	85.4	1674	15	US-10-038-307-17	Sequence 17, Appl1
22	966	85.4	1674	15	US-10-201-292-17	Sequence 17, Appl1
23	966	85.4	1713	15	US-10-038-307-19	Sequence 19, Appl1
24	966	85.4	1713	15	US-10-201-292-19	Sequence 19, Appl1
25	966	85.4	2272	10	US-09-796-753-11	Sequence 11, Appl1
26	966	85.4	2272	15	US-10-038-307-1	Sequence 1, Appl1
27	966	85.4	2272	15	US-10-201-292-1	Sequence 1, Appl1
28	966	85.4	2353	15	US-10-198-846-9957	Sequence 9957, Ap
29	966	85.4	2459	9	US-09-833-381-998	Sequence 998, App
30	966	85.4	5540	13	US-09-918-715-176	Sequence 176, App
31	966	85.4	5540	13	US-09-918-715-231	Sequence 231, App
32	966	85.4	5540	15	US-10-301-822-198	Sequence 198, App
33	960	84.9	5220	13	US-09-918-715-186	Sequence 186, App
34	960	84.9	5220	13	US-09-918-715-300	Sequence 300, App
35	938	82.9	2397	16	US-10-062-674-11757	Sequence 11757, Ap
36	878	77.6	1464	15	US-10-201-292-31	Sequence 31, Appl1
37	767	67.8	1401	15	US-10-201-292-27	Sequence 27, Appl1
38	767	67.8	1401	15	US-10-201-292-29	Sequence 29, Appl1
39	704	62.2	1650	14	US-10-047-542-98	Sequence 98, Appl1
40	704	62.2	6602	14	US-10-047-542-100	Sequence 100, App
41	571	50.5	454	16	US-10-062-674-117	Sequence 417, App
42	534	47.2	569	10	US-09-918-995-22508	Sequence 22508, A
43	506	44.7	977	16	US-10-264-237-169	Sequence 169, App
44	506	44.7	1492	16	US-10-120-988-297	Sequence 297, App
45	506	44.7	2026	16	US-10-094-749-495	Sequence 495, App

## ALIGNMENTS

RESULT 1  
US-10-037-270-8  
; Sequence 8, Application US/10037270  
; Publication No. US20030104529A1  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Asundi, Vinod  
APPLICANT: Zhang, Jie  
APPLICANT: Ren, Feiyan  
APPLICANT: Chen, Rui-hong  
APPLICANT: Zhao, Qing A.  
APPLICANT: Wehtman, Tom  
APPLICANT: Xue, Aidong J.  
APPLICANT: Yang, Yonghong  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Zhou, Ping  
APPLICANT: Ma, Yundong  
APPLICANT: Wang, Dunrui  
APPLICANT: Wang, Zhiwei  
APPLICANT: Tillinghast, John  
APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and

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; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/10/037,270
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pc_fl_genes Version 1.0
; SEQ ID NO 8
; LENGTH: 1609
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (309)..(1202)
; US-10-037-270-8

Alignment Scores:
Pred. No.: 2,11e-145 Length: 1609
Score: 1131.00 Matches: 218
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-970-076-10 (1-218) x US-10-037-270-8 (1-1609)

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Db 546 ATGTCCTTATTTGTTTCTCCACCCGAGAAACACTTAATGAACTGACAGAAACAGA 605

QY 21 GluGlnIleArgGlnGlyLeuGluGluGlnIleValLeuProGlyValAspThrTyr 40
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QY 41 MetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyr 60
Db 666 ATGCATGAAGGATTGAAAGGCCGAGTGAAGCATTTATTATGAAACACAGCAAGGTTAC 725

QY 61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePhe 80
Db 726 AGGACAGCCAGCGTCATCATTTGCTTGTGACTGATGAGAACTCCATGAAGATCTCTTTTTC 785

QY 81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGly 100
Db 786 TATTCAGAGAGGAGGCTAATAGTCTGAGATCTTGCGCAATTTGTTACTGTGTGGT 845

QY 101 ValIysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerTyrAspHisValPhe 120
Db 846 GTGAAGATTTCAATGACACACAGCTGGCCGGATTCGCAAGTAAAGATCATGTGTTT 905

QY 121 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSer 140
Db 906 CCCGGAATGACGCGCTTCAGGCTCTGCAGGCAATCATCCACTCAATTTTGAAGAAGTCC 965

QY 141 CysIleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnVal 160
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QY 161 ValIysAspGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPhe 180
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QY 181 LysIleAsnAspSerValThrLeuSerLysSerLeuGlnSerProTyrValSerSerThr 200
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QY 201 SerGlyPheLysGluGlyAsnSerHisProCysLeuProAlaArgProHisThr 218
Db 1146 AGTGCTTCAAGGAAGGAAATTTCCACCTTGCTTTCAGAGAGGCCACACACA 1199
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RESULT 2
US-10-117-722-8
; Sequence 8, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Zhanmac, Radoje T.
; TITLE OF INVENTION: NO. US20030219744A1el Nucleic Acids and
; FILE REFERENCE: 784CIP2B2CIP
; CURRENT APPLICATION NUMBER: US/10/117,722
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pc_fl_genes Version 1.0
; SEQ ID NO 8
; LENGTH: 1609
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (309)..(1202)
; US-10-117-722-8

Alignment Scores:
Pred. No.: 2,11e-145 Length: 1609
Score: 1131.00 Matches: 218
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

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QY 21 GluGlnIleArgGlnGlyLeuGluGluGlnIleValLeuProGlyValAspThrTyr 40
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QY 41 MetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyr 60
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QY 61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePhe 80
Db 726 AGGACAGCCAGCGTCATCATTTGCTTGTGACTGATGAGAACTCCATGAAGATCTCTTTTTC 785

QY 81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGly 100
Db 786 TATTCAGAGAGGAGGCTAATAGTCTGAGATCTTGCGCAATTTGTTACTGTGTGGT 845

QY 101 ValIysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerTyrAspHisValPhe 120
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161 ValValaArgGlyAenGlyPheAArgHisAlaArgAenValaAArgValLeuCySerPhe 180  
Db 1026 GTCTGGAAGAGAAAGCGCTTCCGACATCCCGACAGCGAGACGGCTCTTGCACGCTTC 1085  
Qy 181 LysIleAenAerSerValThrLeuSerLysSerLeuGlnSerProTPrValSerThr 200  
Db 1086 AAGATCATGACTCGGTGCACACTAGTAAGTCTTGACAGATCCATGGGTTCTTCGACA 1145  
Qy 201 SerGlyPheLysGlyAenSerHisProCyLeuProAlaArgProHisThr 218  
Db 1146 AGTGCTTCAAGAGAGAAATCCACCTTGTCTTCGACAGAGCGCCACACACA 1199

RESULT 3  
US-10-201-292-33  
; Sequence 33, Application US/10201292  
; Publication No. US20030144193A1  
; GENERAL INFORMATION:  
; APPLICANT: James B. ROTTMAN  
; APPLICANT: Theresa L. O'KEEFE  
; APPLICANT: Engin OZKANNAK  
; APPLICANT: Judith J. HEALEY  
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
; FILE REFERENCE: 7853-253-999  
; CURRENT APPLICATION NUMBER: US/10/201,292  
; CURRENT FILING DATE: 2003-02-14  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 1534  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-201-292-33

Alignment Scores:  
Pred. No.: 3,686-124 Length: 1534  
Score: 977.00 Matches: 197  
Percent Similarity: 92.66% Conservative: 5  
Best Local Similarity: 90.37% Mismatches: 8  
Query Match: 86.38% Indels: 8  
DB: 15 Gaps: 3

US-09-970-076-10 (1-218) x US-10-201-292-33 (1-1534)

Qy 1 MetSerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArg 20  
Db 250 ATGTCCTTATTTGTTTCTCCACCGAGAGAACACTTAATGAATGACAGAAAGACAGA 309  
Qy 21 GluGlnIleArgGlnGlyLeuGluGluLeuGlnValLeuProGlyValAspThrTyr 40  
Db 310 GAACAAATCCGTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTAC 369  
Qy 41 MetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyr 60  
Db 370 ATGCATGAAGATTTGAAAGGCGCCAGTGACAGATTTATTAAGAAACAGACAAAGGATC 429  
Qy 61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhe 80  
Db 430 AGGACAGCCAGCGTCATCTTGTCTTGAATGAGAACTCCATGAAGATCTCTTTTTC 489  
Qy 81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCyValGly 100  
Db 490 TATTCAAGAGAGGAGCTTAATAGGTCTCGAATCTTGTCATTTGTTACTGTGTGGT 549  
Qy 101 ValLysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhe 120  
Db 550 GTGAAGATTTCAATGAGACACAGCTGCCCGGATGGCGGACAGTAAGATCATGTGTT 609  
Qy 121 ProValAsnAerGlyPheGlnAlaLeuGlnGlyIleIleHisSerLleLeuLysSer 140  
Db 610 CCCGGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCTCAATTTTGAAGAGATCC 669  
Qy 141 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 160

670 TGATCGAAATTTAGACAGCTGAACCATCCACCTATATGTCAGAGAGATCTTCAAGTT 729  
Qy 161 ValValaArgGlyAenGlyPheAArgHisAlaArgAenValaAArgValLeuCySerPhe 180  
Db 730 GTCTGGAAGAGAAAGCGCTTCCGACATCCCGACAGCGAGACGGCTCTTGCACGCTTC 789  
Qy 181 LysIleAenAerSerValThrLeuSerLysSerLeuGlnSerProTPrValSerThr 200  
Db 790 AAGATCATGACTCGGTGCACACTCATATGAGAAAGCCCTTCTCCCAAATC----- 840  
Qy 201 SerGlyPheLysGlyAenSerHisProCyLeuProAlaArgProHisThr 218  
Db 841 -----TTTCGACAA-----AACTCACAC-----ATGCCACCGGTCCAGCACC 879

RESULT 4  
US-10-201-292-35  
; Sequence 35, Application US/10201292  
; Publication No. US20030144193A1  
; GENERAL INFORMATION:  
; APPLICANT: James B. ROTTMAN  
; APPLICANT: Theresa L. O'KEEFE  
; APPLICANT: Engin OZKANNAK  
; APPLICANT: Judith J. HEALEY  
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
; FILE REFERENCE: 7853-253-999  
; CURRENT APPLICATION NUMBER: US/10/201,292  
; CURRENT FILING DATE: 2003-02-14  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35  
; LENGTH: 1608  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-201-292-35

Alignment Scores:  
Pred. No.: 1,126-122 Length: 1608  
Score: 966.50 Matches: 194  
Percent Similarity: 93.18% Conservative: 11  
Best Local Similarity: 88.18% Mismatches: 11  
Query Match: 85.46% Indels: 5  
DB: 15 Gaps: 2

US-09-970-076-10 (1-218) x US-10-201-292-35 (1-1608)

Qy 1 MetSerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArg 20  
Db 250 ATGTCCTTATTTGTTTCTCCACCGAGAGAACACTTAATGAATGACAGAAAGACAGA 309  
Qy 21 GluGlnIleArgGlnGlyLeuGluGluLeuGlnValLeuProGlyValAspThrTyr 40  
Db 310 GAACAAATCCGTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTAC 369  
Qy 41 MetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyr 60  
Db 370 ATGCATGAAGATTTGAAAGGCGCCAGTGACAGATTTATTAAGAAACAGACAAAGGATC 429  
Qy 61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhe 80  
Db 430 AGGACAGCCAGCGTCATCTTGTCTTGAATGAGAACTCCATGAAGATCTCTTTTTC 489  
Qy 81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCyValGly 100  
Db 490 TATTCAAGAGAGGAGCTTAATAGGTCTCGAATCTTGTCATTTGTTACTGTGTGGT 549  
Qy 101 ValLysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhe 120  
Db 550 GTGAAGATTTCAATGAGACACAGCTGCCCGGATGGCGGACAGTAAGATCATGTGTT 609  
Qy 121 ProValAsnAerGlyPheGlnAlaLeuGlnGlyIleIleHisSerLleLeuLysSer 140  
Db 610 CCCGGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCTCAATTTTGAAGAGATCC 669

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OY 141 CysIleGluIleLeuAlaIaGluProSerThrIleCysAlaGlyGluSerPheGlnVal 160
DB 670 TGCATCGAAATTTCTAGCAGCTGAACCACTCCACCATATGTGACAGAGATCTTTCAAGTT 729
OY 161 ValValaArgGlyAanglyPheArgHisAlaArgAsnValaAspArgValleuCysSerPhe 180
DB 730 GTCTGAGAGAGAAACGGCTTCCGACATCCCGCAAGTGCACAGGCTCTCTGCAGCTTC 789
OY 181 LysIleAsnAspSerValThrIleuSerLys-----SerLeuGlnSerProTyrVal 197
DB 790 AAGATCAATGACTCGCTCACTCACTCAATGAAAGCCCTTTCTGTGAAAGATCTTATT- 848
OY 198 SerSerThrSerGlyPheLysGluGlyAanSerHis---ProCysLeuProAlaArgPro 216
DB 849 ACTGTCTCAGCGCTTACTTCTTAAGAAGTTGGCATGAAGCTGCACCTCAGGTCCAGCCC 908

RESULT 5
US-10-038-307-25
; Sequence 25, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-25

Alignment Scores:
Pred. No.: 6,356-123 Length: 1008
Score: 966.00 Matches: 188
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 98.95% Mismatches: 0
Query Match: 85.41% Indels: 0
DB: 15 Gaps: 0

US-09-970-076-10 (1-218) x US-10-038-307-25 (1-1008)
OY 1 MetSerPheIleValPheSerThrArgGlyThrThrIleuMetLysLeuThrGluAspArg 20
DB 250 ATGTCCTTATTTGTTTCTCCACCGAGAGAACCACTTAATGAAGTGAAGAGACAGA 309
OY 21 GluGlnIleArgGlnGlyLeuGluGluLeuGlnLysValleuProGlyGlyAspThrTyr 40
DB 310 GAACAAATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCCAGGAGAGACACTTAC 369
OY 41 MetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyr 60
DB 370 ATGCATGAAGATTGGAAGAGCCCGACAGTGAATTTATGAAAAACAGCAAGGATAC 429
OY 61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePhe 80
DB 430 AGGACAGCCAGCGTCATCATCTTGTGACTGATGAGAACTCCATGAAGATCTCTTTTC 489
OY 81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyValaIleValTyrCysValGly 100
DB 490 TATTTCAGAGAGGAGGCTTAATAGCTCTGAGATCTTGCAATTTGTTACTGTGTGGT 549
OY 101 ValLysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValaPhe 120
DB 550 GTGAAAGATTTTCATGAGACACAGCTGCGCCGATGCGGACAGTAAAGATCATGTGTTT 609
OY 121 ProValaAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSer 140
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DB 610 CCCGTGAATGACGGCTTTCAGGCTTGCAAGGATCATCTCACTCAATTTGAAGAACTCC 669
OY 141 CysIleGluIleLeuAlaIaGluProSerThrIleCysAlaGlyGluSerPheGlnVal 160
DB 670 TGCATCGAAATTTCTAGCAGCTGAACCACTCCACCATATGTGACAGAGATCTTTCAAGTT 729
OY 161 ValValaArgGlyAanglyPheArgHisAlaArgAsnValaAspArgValleuCysSerPhe 180
DB 730 GTCTGAGAGAGAAACGGCTTCCGACATCCCGCAAGTGCACAGGCTCTCTGCAGCTTC 789
OY 181 LysIleAsnAspSerValThrIleuSerLys 190
DB 790 AAGATCAATGACTCGGTCACTCACTCAATGAG 819

RESULT 6
US-10-201-292-25
; Sequence 25, Application US/10201292
; Publication No. US2003014193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-25

Alignment Scores:
Pred. No.: 6,356-123 Length: 1008
Score: 966.00 Matches: 188
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 98.95% Mismatches: 0
Query Match: 85.41% Indels: 0
DB: 15 Gaps: 0

US-09-970-076-10 (1-218) x US-10-201-292-25 (1-1008)
OY 1 MetSerPheIleValPheSerThrArgGlyThrThrIleuMetLysLeuThrGluAspArg 20
DB 250 ATGTCCTTATTTGTTTCTCCACCGAGAGAACCACTTAATGAAGTGAAGAGACAGA 309
OY 21 GluGlnIleArgGlnGlyLeuGluGluLeuGlnLysValleuProGlyGlyAspThrTyr 40
DB 310 GAACAAATCCGTCAAGGCTTAGAAGAACTCCAGAAAGTTCTGCCAGGAGAGACACTTAC 369
OY 41 MetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyr 60
DB 370 ATGCATGAAGATTGGAAGAGCCCGACAGTGAATTTATGAAAAACAGCAAGGATAC 429
OY 61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePhe 80
DB 430 AGGACAGCCAGCGTCATCATCTTGTGACTGATGAGAACTCCATGAAGATCTCTTTTC 489
OY 81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyValaIleValTyrCysValGly 100
DB 490 TATTTCAGAGAGGAGGCTTAATAGCTCTCGAGATCTTGTCATTTGTTACTGTGTGGT 549
OY 101 ValLysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValaPhe 120
DB 550 GTGAAAGATTTTCATGAGACACAGCTGCGCCGATGCGGACAGTAAAGATCATGTGTTT 609
OY 121 ProValaAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSer 140
DB 610 CCGTGATGACGGCTTTCAGGCTTGCAAGGATCATCTCACTCAATTTGAAGAACTCC 669
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141 CysilegllleleuAlaIaIgluProserThrlleCyAlaIgluSerPhegluVal 160  
Db 670 TGCATCGAAATTTCTAGCAGCTGACCACTCCATATGTCAGGAGCTCTTCAAGTT 729  
Qy 161 ValValaIargIyAaNgIyPheArghIaIaIargAenValaIaPargValleuCySerPhe 180  
Db 730 GTCGTGAGAGGAAACGGCTTCGACATGCCGCAACGTGACAGGGCTCTCTGACGCTTC 789  
Qy 181 LysIleAaenAaSerValThrlleuSerLys 190  
Db 790 AAGATCAATGACTCGGTCACTCACTCAATGAG 819

RESULT 7  
US-10-038-307-21  
; Sequence 21, Application US/10038307  
; Publication No. US20030134786A1  
; GENERAL INFORMATION:  
; APPLICANT: James B. ROTTMAN  
; APPLICANT: Theresa L. O'KEEFE  
; APPLICANT: Engin OZKAYNAK  
; APPLICANT: Judith J. HEALEY  
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
; FILE REFERENCE: 7853-253-999  
; CURRENT APPLICATION NUMBER: US/10/038,307  
; CURRENT FILING DATE: 2002-06-28  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 1047  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-038-307-21

Alignment Scores:  
Pred. No.: 6,73e-123 Length: 1047  
Score: 966.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 98.95% Mismatches: 0  
Query Match: 85.41% Indels: 0  
DB: 15 Gaps: 0

US-09-970-076-10 (1-218) x US-10-038-307-21 (1-1047)

Qy 1 MetSerPheIleValIaPheSerThrArgIyThrlleuMeLyLeuThrluAaParg 20  
Db 277 ATGTCCTTATGTTTCTCCACCCGAGAACACTTAATGAATACTGACGAAAGACAGA 336  
Qy 21 GluGlnIleArgGlnGlyLeuGlnIleuGlnIleuValleuProGlyGlyAaPthTyr 40  
Db 337 GAACAATCCGTCAAGGCTAGAAAGACTCCGAAAGTTCTGCCAGAGAGACACTTAC 396  
Qy 41 MethIeGluGlyPheGluAaIaSerGluGlnIleTyrTyrGluAaAaArgGlnIyTyr 60  
Db 397 ATGCATGAAGATTTGAAAGGCGCAGTGACAGATTATTAAGAAACAGACAGGGTAC 456  
Qy 61 ArgThrAlaSerValIleIleAlaLeuThraPargIyGluLeuHlgIuAaPleuPhe 80  
Db 457 AGGACAGCCAGCGTCATCATCTTGTGACTGATGGAAGTCACTCAAGATCTCTTTTC 516  
Qy 81 TyrSerGluArgGluAlaAaAaSerArgAaPleuGlyAlaIleValTyrCyValaGly 100  
Db 517 TATTCAGAGAGGAGGCTTAATAGGTCGAGATCTTGCGCAATGTTTACTGTGTGCT 576  
Qy 101 ValIyAaPheAaNgIyThrlleuAlaIaIgluAaIaArgIleAlaAaPserLysAaPhe 120  
Db 577 GTGAAGATTTCAATGACACACAGCTGCGCGGATTCGCGACATGAAGATCATGTGTT 636  
Qy 121 ProValAaAaPargIyPheGlnAlaIeugInGlyIleIleHlgIuSerIleLeuLysSer 140  
Db 637 CCCGGAATGACGGCTTCAAGCTCTGCAAGGATCTCACTCAATTTTGAAGAGTCC 696  
Qy 141 CysIleGluIleleuAlaIaIgluProserThrlleCyAlaIgluSerPhegluVal 160

Db 697 TGCATCGAAATTTCTAGCAGCTGACCACTCCATATGTCAGGAGCTCTTCAAGTT 756  
Qy 161 ValValaIargIyAaNgIyPheArghIaIaIargAenValaIaPargValleuCySerPhe 180  
Db 757 GTCGTGAGAGGAAACGGCTTCGACATGCCGCAACGTGACAGGGCTCTCTGACGCTTC 816  
Qy 181 LysIleAaenAaSerValThrlleuSerLys 190  
Db 817 AAGATCAATGACTCGGTCACTCACTCAATGAG 846

RESULT 8  
US-10-201-292-21  
; Sequence 21, Application US/10201292  
; Publication No. US20030144193A1  
; GENERAL INFORMATION:  
; APPLICANT: James B. ROTTMAN  
; APPLICANT: Theresa L. O'KEEFE  
; APPLICANT: Engin OZKAYNAK  
; APPLICANT: Judith J. HEALEY  
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
; FILE REFERENCE: 7853-253-999  
; CURRENT APPLICATION NUMBER: US/10/201,292  
; CURRENT FILING DATE: 2003-02-14  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 1047  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-201-292-21

Alignment Scores:  
Pred. No.: 6,73e-123 Length: 1047  
Score: 966.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 98.95% Mismatches: 0  
Query Match: 85.41% Indels: 0  
DB: 15 Gaps: 0

US-09-970-076-10 (1-218) x US-10-201-292-21 (1-1047)

Qy 1 MetSerPheIleValIaPheSerThrArgIyThrlleuMeLyLeuThrluAaParg 20  
Db 277 ATGTCCTTATGTTTCTCCACCCGAGAACACTTAATGAATACTGACGAAAGACAGA 336  
Qy 21 GluGlnIleArgGlnGlyLeuGlnIleuGlnIleuValleuProGlyGlyAaPthTyr 40  
Db 337 GAACAATCCGTCAAGGCTAGAAAGACTCCGAAAGTTCTGCCAGAGAGACACTTAC 396  
Qy 41 MethIeGluGlyPheGluAaIaSerGluGlnIleTyrTyrGluAaAaArgGlnIyTyr 60  
Db 397 ATGCATGAAGATTTGAAAGGCGCAGTGACAGATTATTAAGAAACAGACAGGGTAC 456  
Qy 61 ArgThrAlaSerValIleIleAlaLeuThraPargIyGluLeuHlgIuAaPleuPhe 80  
Db 457 AGGACAGCCAGCGTCATCATCTTGTGACTGATGGAAGTCACTCAAGATCTCTTTTC 516  
Qy 81 TyrSerGluArgGluAlaAaAaSerArgAaPleuGlyAlaIleValTyrCyValaGly 100  
Db 517 TATTCAGAGAGGAGGCTTAATAGGTCGAGATCTTGCGCAATGTTTACTGTGTGCT 576  
Qy 101 ValIyAaPheAaNgIyThrlleuAlaIaIgluAaIaArgIleAlaAaPserLysAaPhe 120  
Db 577 GTGAAGATTTCAATGACACACAGCTGCGCGGATTCGCGACATGAAGATCATGTGTT 636  
Qy 121 ProValAaAaPargIyPheGlnAlaIeugInGlyIleIleHlgIuSerIleLeuLysSer 140  
Db 637 CCCGGAATGACGGCTTCAAGCTCTGCAAGGATCTCACTCAATTTTGAAGAGTCC 696  
Qy 141 CysIleGluIleleuAlaIaIgluProserThrlleCyAlaIgluSerPhegluVal 160  
Db 697 TGCATCGAAATTTCTAGCAGCTGACCACTCCATATGTCAGGAGCTCTTCAAGTT 756

Qy 161 ValValArgGlyAenglyPheargHisAlaArgAenValAspArgValIleuCySerPhe 180  
Db 757 GTCGTGAGAGGAAGCGCTTCGACATGCCCGAAGCGTGAAGGCTCTCTGACGCTTC 816  
Qy 181 LysIleAsnAspSerValThrIleuSerLys 190  
Db 817 AAGATCAATGACTCGGTCACTCACTCAATGAG 846

RESULT 9  
US-10-038-307-23  
; Sequence 23, Application US/10038307  
; Publication No. US20030134786A1  
; GENERAL INFORMATION:  
; APPLICANT: James B. ROTTMAN  
; APPLICANT: Theresa L. O'KEEFE  
; APPLICANT: Engin OZKANAK  
; APPLICANT: Judith J. HEALEY  
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
; FILE REFERENCE: 7853-253-999  
; CURRENT FILING DATE: 2002-06-28  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 1056  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-038-307-23

Alignment Scores:  
Pred. No.: 6,82e-123 Length: 1056  
Score: 966.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 98.95% Mismatches: 0  
Query Match: 85.41% Indels: 0  
Gaps: 0

US-09-970-076-10 (1-218) x US-10-038-307-23 (1-1056)

Qy 1 MetSerPheIleValPheSerThrArgGlyThrThrIleuMetLysLeuThrGluAspArg 20  
Db 250 ATGTCCTTATTTGTTTCTCCACCGAGAAACMACTTAATGAACCTGACGAAGACGA 309  
Qy 21 GluGlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyr 40  
Db 310 GAACAAATCCCTCAAGGCTTGAAGAAGCTCCGAAGTTCTGCCAGGAGAGACACTTAC 369  
Qy 41 MetHisGlnGlyPheGluArgAlaSerGlnIleTyrTyrGluAsnArgGlnGlyTyr 60  
Db 370 ATGCATGAAGATTGAAAGGCGCAGTGAGCAGATTATTATGAAAACAGCAAGGCTAC 429  
Qy 61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePhe 80  
Db 430 AGGACAGCCAGGCTCATCTGCTTGACTGATGAGAACTCCAGAAAGATCTCTTTTC 489  
Qy 81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGly 100  
Db 490 TATTACAGAGGAGGAGCTTAATAGCTCTGAGATCTTGTCGAATTTGTTACTGTGTTG 549  
Qy 101 ValIysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhe 120  
Db 550 GTGAAGAATTTCAATGAGACACAGCTGCCGAGATTGCCAGATGAGATCATGTGTTT 609  
Qy 121 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSer 140  
Db 610 CCCGTGAATGACGGCTTTCAGGCTTGCAGAGCATCATCACTCAATTTTGAAGAAGTCC 669  
Qy 141 CysIleGlnIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnVal 160  
Db 670 TGATCGAAATTTCTAGACGCTGAACCATCCACCATATGTGAGGAGGACTTTCATGTT 729  
Qy 161 ValValArgGlyAenglyPheargHisAlaArgAenValAspArgValIleuCySerPhe 180

Db 730 GTCGTGAGAGGAAGCGCTTCGACATGCCCGAAGCGTGAAGGCTCTCTGACGCTTC 789  
Qy 181 LysIleAsnAspSerValThrIleuSerLys 190  
Db 790 AAGATCAATGACTCGGTCACTCACTCAATGAG 819

RESULT 10  
US-10-201-292-23  
; Sequence 23, Application US/10201292  
; Publication No. US2003014193A1  
; GENERAL INFORMATION:  
; APPLICANT: James B. ROTTMAN  
; APPLICANT: Theresa L. O'KEEFE  
; APPLICANT: Engin OZKANAK  
; APPLICANT: Judith J. HEALEY  
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
; FILE REFERENCE: 7853-253-999  
; CURRENT FILING DATE: 2003-02-14  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 1056  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-201-292-23

Alignment Scores:  
Pred. No.: 6,82e-123 Length: 1056  
Score: 966.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 98.95% Mismatches: 0  
Query Match: 85.41% Indels: 0  
Gaps: 0

US-09-970-076-10 (1-218) x US-10-201-292-23 (1-1056)

Qy 1 MetSerPheIleValPheSerThrArgGlyThrThrIleuMetLysLeuThrGluAspArg 20  
Db 250 ATGTCCTTATTTGTTTCTCCACCGAGAAACMACTTAATGAACCTGACGAAGACGA 309  
Qy 21 GluGlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyr 40  
Db 310 GAACAAATCCCTCAAGGCTTGAAGAAGCTCCGAAGTTCTGCCAGGAGAGACACTTAC 369  
Qy 41 MetHisGlnGlyPheGluArgAlaSerGlnGlnIleTyrTyrGluAsnArgGlnGlyTyr 60  
Db 370 ATGCATGAAGATTGAAAGGCGCAGTGAGCAGATTATTATGAAAACAGCAAGGCTAC 429  
Qy 61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePhe 80  
Db 430 AGGACAGCCAGGCTCATCTGCTTGACTGATGAGAACTCCAGAAAGATCTCTTTTC 489  
Qy 81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGly 100  
Db 490 TATTACAGAGGAGGAGCTTAATAGCTCTGAGATCTTGTCGAATTTGTTACTGTGTTG 549  
Qy 101 ValIysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhe 120  
Db 550 GTGAAGAATTTCAATGAGACACAGCTGCCGAGATTGCCAGATGAGATCATGTGTTT 609  
Qy 121 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSer 140  
Db 610 CCCGTGAATGACGGCTTTCAGGCTTGCAGAGCATCATCACTCAATTTTGAAGAAGTCC 669  
Qy 141 CysIleGlnIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnVal 160  
Db 670 TGATCGAAATTTCTAGACGCTGAACCATCCACCATATGTGAGGAGGACTTTCATGTT 729  
Qy 161 ValValArgGlyAenglyPheargHisAlaArgAenValAspArgValIleuCySerPhe 180  
Db 730 GTCGTGAGAGGAAGCGCTTCGACATGCCCGAAGCGTGAAGGCTCTCTGACGCTTC 789



QY 181 LysileAsnAspSerValThrLeuSerLys 190  
DB 790 AAGATCAATGACTCGTCACTCAATGAG 819

RESULT 11  
US-10-133-937-58  
Sequence 58, Application US/10133937  
Publication No. US20030207278A1  
GENERAL INFORMATION:  
APPLICANT: Khan, Javed  
APPLICANT: Ringner, Markus  
APPLICANT: Peterson, Carsten  
APPLICANT: Meltzer, Paul  
TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING, DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND  
FILE REFERENCE: 11613.56US01  
CURRENT APPLICATION NUMBER: US/10/133,937  
PRIORITY FILING DATE: 2002-11-04  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 58  
LENGTH: 1454  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-133-937-58

Alignment Scores:  
Pred. No.: 1.12e-122 Length: 1454  
Score: 966.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 98.95% Mismatches: 0  
Query Match: 85.41% Indels: 0  
Gaps: 0  
DB: 16

US-09-970-076-10 (1-218) x US-10-133-937-58 (1-1454)

QY 1 MetSerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArg 20  
DB 381 ATGTCCTTATTTGTTTCTCCACCCGAGGACCACTTAAATGAACTGACAGAAACAGCA 440

QY 21 GluGlnIleArgGlnGlyLeuGluGluLeuGlnLysValLeuProGlyGlyAspThrTyr 40  
DB 441 GAACAAATCCGTCAGAGGCTTGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTAC 500

QY 41 MetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyr 60  
DB 501 ATGCATGAAGATTTGAAAGGCGCAGTGACAGATTATTATGAAACAGACAGAGGTAC 560

QY 61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePhe 80  
DB 561 AGGACAGCCAGCGTCATCTGCTTGAAGTGAAGAACTCATGAAAGATCTCTTTTTC 620

QY 81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGly 100  
DB 621 TATTACAGAGGAGGAGCTTAATAGGTCGAGATCTTGCGCAATGTTTACTGTGTGTT 680

QY 101 ValIysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhe 120  
DB 681 GTGAAGATTTCAATGAGACACAGCTGCCCGGATTTGGGACAGTAAGATCATGTGTTT 740

QY 121 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSer 140  
DB 741 CCCGTAATGACGGCTTTCAGGCTCTGCAAGGATCATCTCAATTTTGAAGAGTCC 800

QY 141 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 160  
DB 801 TGCATCGAAATTTCTAGCAGCTGAACCATCACCATTATGTGACAGAGATCATTTCAAGTT 860

QY 161 ValIleArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPhe 180  
DB 861 GTCGTGAGAGGAAAGGCTTCCGACATGCTCCCAAGCTGAGACAGGCTCTCTGCAAGCTTC 920

QY 181 LysileAsnAspSerValThrLeuSerLys 190  
DB 921 AAGATCAATGACTCGTCACTCAATGAG 950

RESULT 12  
US-10-159-563-58  
Sequence 58, Application US/10159563  
Publication No. US20040009154A1  
GENERAL INFORMATION:  
APPLICANT: Khan, Javed  
APPLICANT: Ringner, Markus  
APPLICANT: Peterson, Carsten  
APPLICANT: Meltzer, Paul  
TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
FILE REFERENCE: 11613.56US11  
CURRENT APPLICATION NUMBER: US/10/159,563  
PRIORITY FILING DATE: 2002-12-09  
CURRENT APPLICATION NUMBER: US 10/133,937  
PRIOR FILING DATE: 2002-04-25  
NUMBER OF SEQ ID NOS: 444  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 58  
LENGTH: 1454  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-159-563-58

Alignment Scores:  
Pred. No.: 1.12e-122 Length: 1454  
Score: 966.00 Matches: 188  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 98.95% Mismatches: 0  
Query Match: 85.41% Indels: 0  
Gaps: 0  
DB: 16

US-09-970-076-10 (1-218) x US-10-159-563-58 (1-1454)

QY 1 MetSerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArg 20  
DB 381 ATGTCCTTATTTGTTTCTCCACCCGAGGACCACTTAAATGAACTGACAGAAACAGCA 440

QY 21 GluGlnIleArgGlnGlyLeuGluGluLeuGlnLysValLeuProGlyGlyAspThrTyr 40  
DB 441 GAACAAATCCGTCAGAGGCTTGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTAC 500

QY 41 MetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyr 60  
DB 501 ATGCATGAAGATTTGAAAGGCGCAGTGACAGATTATTATGAAACAGACAGAGGTAC 560

QY 61 ArgThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePhe 80  
DB 561 AGGACAGCCAGCGTCATCTGCTTGAAGTGAAGAACTCATGAAAGATCTCTTTTTC 620

QY 81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGly 100  
DB 621 TATTACAGAGGAGGAGCTTAATAGGTCGAGATCTTGCGCAATGTTTACTGTGTGTT 680

QY 101 ValIysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhe 120  
DB 681 GTGAAGATTTCAATGAGACACAGCTGCCCGGATTTGGGACAGTAAGATCATGTGTTT 740

QY 121 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSer 140  
DB 741 CCCGTAATGACGGCTTTCAGGCTCTGCAAGGATCATCTCAATTTTGAAGAGTCC 800

QY 141 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnVal 160  
DB 801 TGCATCGAAATTTCTAGCAGCTGAACCATCACCATTATGTGACAGAGATCATTTCAAGTT 860

QY 161 ValIleArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPhe 180

Db 861 GTCGTGAGAGAAACGGCTTCGACATCCCGCAACGTGACAGGGTCTCTGCAGCTTC 920  
Qy 181 LysilleaenApservAlThrluSerLys 190  
Db 921 AAGATCAATGACTCGGTCACTCAATGAG 950

## RESULT 13

US-10-038-307-11  
; Sequence 11, Application US/10038307  
; Publication No. US20030134786A1  
; GENERAL INFORMATION:  
; APPLICANT: James B. ROTTMAN  
; APPLICANT: Theresa L. O'KEEFE  
; APPLICANT: Engin OZKAYNAK  
; APPLICANT: Judith J. HEALEY  
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
; FILE REFERENCE: 7853-253-999  
; CURRENT APPLICATION NUMBER: US/10/038,307  
; CURRENT FILING DATE: 2002-06-28  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 1623  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-038-307-11

## Alignment Scores:

Pred. No.:	1,338-122	Length:	1623
Score:	966.00	Matches:	188
Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	98.95%	Mismatches:	0
Query Match:	85.41%	Indels:	0
DB:	15	Gaps:	0

US-09-970-076-10 (1-218) x US-10-038-307-11 (1-1623)

Qy 1 MetSerPheIleValPheSerThrArgGlyThrThrluMetLysLeuThrgluApsArg 20  
Db 211 ATGTCCTTATTGTTTCTCCACCCGAGAACAACTTAATGAACTGACAGAAAGACGA 270  
Qy 21 GluGlnIleArgGlnGlyLeuGluGluLeuGlnLysValLeuProGlyGlyApsThrTyr 40  
Db 271 GAACAAATCCGTCAGAGGCTAGAAAGACTCCAGAAAGTTCTCCGAGGAGACACTTAC 330  
Qy 41 MetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluApsArgGlnGlyTyr 60  
Db 331 ATGCATGAAGATTGAAAGGCCAGTGAAGCATTTATTGAAAGACAGACAGGATAC 390  
Qy 61 ArgThrAlaSerValIleIleAlaLeuThrApsGlyGluLeuHisGluApsLeuPhePhe 80  
Db 391 AGGACAGCCAGCGTCATCTGCTTGACTGAGAACTCCAGAACTCATGAAATCTCTTTTTC 450  
Qy 81 TyrSerGluArgGluAlaAsnArgSerArgApsLeuGlyAlaIleValTyrCyValGly 100  
Db 451 TATTCAAGAGAGGAGCTAATAGGTCCTGAGATCTTGGTCTATTGTTACTGTGTGGT 510  
Qy 101 ValLysApsPheApsGluThrglnLeuAlaArgIleAlaApsSerLysApsHisValPhe 120  
Db 511 GTGAAAGATTTCAATGAGACACAGCTGGCCGAGATTGCGAGACATGAGATCATGTGTTT 570  
Qy 121 ProValAsnApsGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSer 140  
Db 571 CCCCGAATGACGCTTCAAGCTCTGCAAGCATCATCACTCAATTTTGAAGAATCC 630  
Qy 141 CysIleGluIleLeuAlaAlaGluProSerThrIleCyValAGlyGluSerPheGlnVal 160  
Db 631 TGCAATCAAAATTTCTGACAGCTGAACCATCCCAATATGTGACGAGACTCATTTCAAGTT 690  
Qy 161 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValApsArgValLeuCySerPhe 180  
Db 691 GTGCTGAGAGAAACGGCTTCGACATGCCGCAACGTGACAGGGTCTCTGACAGCTTC 750

Qy 181 LysilleaenApservAlThrluSerLys 190  
Db 751 AAGATCAATGACTCGGTCACTCAATGAG 780

## RESULT 14

US-10-201-292-11  
; Sequence 11, Application US/10201292  
; Publication No. US2003014193A1  
; GENERAL INFORMATION:  
; APPLICANT: James B. ROTTMAN  
; APPLICANT: Theresa L. O'KEEFE  
; APPLICANT: Engin OZKAYNAK  
; APPLICANT: Judith J. HEALEY  
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
; FILE REFERENCE: 7853-253-999  
; CURRENT APPLICATION NUMBER: US/10/201,292  
; CURRENT FILING DATE: 2003-02-14  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 1623  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-201-292-11

## Alignment Scores:

Pred. No.:	1,338-122	Length:	1623
Score:	966.00	Matches:	188
Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	98.95%	Mismatches:	0
Query Match:	85.41%	Indels:	0
DB:	15	Gaps:	0

US-09-970-076-10 (1-218) x US-10-201-292-11 (1-1623)

Qy 1 MetSerPheIleValPheSerThrArgGlyThrThrluMetLysLeuThrgluApsArg 20  
Db 211 ATGTCCTTATTGTTTCTCCACCCGAGAACAACTTAATGAACTGACAGAAAGACGA 270  
Qy 21 GluGlnIleArgGlnGlyLeuGluGluLeuGlnLysValLeuProGlyGlyApsThrTyr 40  
Db 271 GAACAAATCCGTCAGAGGCTAGAAAGACTCCAGAAAGTTCTCCGAGGAGACACTTAC 330  
Qy 41 MetHisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluApsArgGlnGlyTyr 60  
Db 331 ATGCATGAAGATTGAAAGGCCAGTGAAGCATTTATTGAAAGACAGACAGGATAC 390  
Qy 61 ArgThrAlaSerValIleIleAlaLeuThrApsGlyGluLeuHisGluApsLeuPhePhe 80  
Db 391 AGGACAGCCAGCGTCATCTGCTTGACTGAGAACTCCAGAACTCATGAAATCTCTTTTTC 450  
Qy 81 TyrSerGluArgGluAlaAsnArgSerArgApsLeuGlyAlaIleValTyrCyValGly 100  
Db 451 TATTCAAGAGAGGAGCTAATAGGTCCTGAGATCTTGGTCTATTGTTACTGTGTGGT 510  
Qy 101 ValLysApsPheApsGluThrglnLeuAlaArgIleAlaApsSerLysApsHisValPhe 120  
Db 511 GTGAAAGATTTCAATGAGACACAGCTGGCCGAGATTGCGAGACATGAGATCATGTGTTT 570  
Qy 121 ProValAsnApsGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSer 140  
Db 571 CCCCGAATGACGCTTCAAGCTCTGCAAGCATCATCACTCAATTTTGAAGAATCC 630  
Qy 141 CysIleGluIleLeuAlaAlaGluProSerThrIleCyValAGlyGluSerPheGlnVal 160  
Db 631 TGCAATCAAAATTTCTGACAGCTGAACCATCCCAATATGTGACGAGACTCATTTCAAGTT 690  
Qy 161 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValApsArgValLeuCySerPhe 180  
Db 691 GTGCTGAGAGAAACGGCTTCGACATGCCGCAACGTGACAGGGTCTCTGACAGCTTC 750

Db 751 AAGATCAATGACTCGTCACACTCAATGAG 780

## RESULT 15

US-10-038-307-9

/ Sequence 9, Application US/10038307  
/ Publication No. US20030134786A1

/ GENERAL INFORMATION:

/ APPLICANT: James B. ROTTMAN

/ APPLICANT: Theresa L. O'KEEFE

/ APPLICANT: Englin OZKANAK

/ APPLICANT: Judith J. HEALEY

/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

/ FILE REFERENCE: 7853-253-999

/ CURRENT APPLICATION NUMBER: US/10/038,307

/ CURRENT FILING DATE: 2002-06-28

/ NUMBER OF SEQ ID NOS: 26

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 9

/ LENGTH: 1650

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-10-038-307-9

## Alignment Scores:

Pred. No.:	1,366-122	Length:	1650
Score:	966.00	Matches:	188
Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	98.95%	Mismatches:	0
Query Match:	85.41%	Indels:	0
DB:	15	Gaps:	0

US-09-970-076-10 (1-218) x US-10-038-307-9 (1-1650)

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QY      1 MetSerPheIleValPheSerThrArgGlyThrThrLeuMetIleuThrGluAspArg 20
        |||||
Db      238 ATGTCCTTATTTGTTTCTCCACCCGAGGACMACCTTAATGAACTGACAGAGACAGA 297
QY      21 GluGlnIleArgGlnGlyLeuGlnGluLeuGlnIleuValIleuProGlyGlyAspThrTyr 40
        |||||
Db      298 GAACTAATCCGTCAGAGCCCTAGAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTAC 357
QY      41 MetHisGluGlyPheGluArgHisSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyr 60
        |||||
Db      358 ATGCATGAAGATTGAAAGGCCCAAGTGAAGATTTATTAAGAAACGACCAAGGTAC 417
QY      61 ArgThrAlaSerValIleIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePhe 80
        |||||
Db      418 AGGACAGCCAGCGTCATCATTCCTTGACTGATGAGAACTCCATGAAGATCTCTTTTC 477
QY      81 TyrSerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGly 100
        |||||
Db      478 TATTGAGAGAGGAGGCTTAATAGGTCTCGAGATCTTGCGCAATGTTACTGTGTGCT 537
QY      101 ValIleAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerIleAspHisValPhe 120
        |||||
Db      538 GTGAAGAATTTCATGAGACACAGCTGCGCCGATTCGCGACAGTAAGATCATGTCTTT 597
QY      121 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIleValSer 140
        |||||
Db      598 CCGCGAATGACGCGCTTCAGGCTCTGCAAGGCATCATCCACTCAATTTTGAAAGATCC 657
QY      141 CysIleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnVal 160
        |||||
Db      658 TGCATCGAATTTCTAGCAGCTGACCAATCCATATGTCAGAGAGTCATTTCAAGTT 717
QY      161 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPhe 180
        |||||
Db      718 GTCCGAGAGGAAAGCGCTTCGACATGCGCGCAACGTGACAGGCTCCTCGACGCTTC 777
QY      181 LysIleAsnAspSerValThrLeuSerIle 190
        |||||
Db      778 AAGATCAATGACTCGTCACACTCAATGAG 807
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Search completed: June 22, 2004, 08:11:33  
Job time : 329.721 secs

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Db 205 TEFKSSLSQSLVDIAIVQLQ-----GLTYTASGIQKVKELEFHSNGARKSAKKILIVIT 259  
QY 71 DGEIHEDLFFYSE--REANRSRDGAIVYCVGVD-FNE-TOLARI-----ADSKDHVP 121  
Db 260 DGQKFRDPLEYRHVYIPEAKA---GIRYALGVDAFREPALDELNTIGSAPSQDHVPK 316  
QY 122 VNDGFOLQGIHSLKSCIEILAAEPSTICAGESFOVVVRGNGFPHARNVD 174  
Db 317 VGN-FVALRSIORQIOEK-----IFAIEGTESRSSSSFOHEMSQGFSSALSM 364

RESULT 2  
US-08-485-618-46  
; Sequence 46, Application US/08485618  
; Patent No. 5728533  
; GENERAL INFORMATION:  
; APPLICANT: Gallatin, W. Michael  
; APPLICANT: Van der Vlieten, Monica  
; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 South Wacker Drive, 6300 Sear Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485.618  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/173,497  
; FILING DATE: 23-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/286,889  
; FILING DATE: 5-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/362,652  
; FILING DATE: 21-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams Jr., Joseph A.  
; REGISTRATION NUMBER: 38,659  
; REFERENCE/DOCKET NUMBER: 27866/32797  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; TELEFAX: 312-474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 46:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1155 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-485-618-46

Query Match 11.4%; Score 128.5; DB 1; Length 1155;  
Best Local Similarity 28.9%; Pred. No. 1.2e-05;  
Matches 50; Conservative 31; Mismatches 69; Indels 23; Gaps 9;  
QY 12 TLMKLTEDREQIRGLBELQKVLPGDPTVMHEGFRASEQIYYENRGYRTA-SVIALT 70  
Db 205 TEFKSSLSQSLVDIAIVQLQ-----GLTYTASGIQKVKELEFHSNGARKSAKKILIVIT 259  
QY 71 DGEIHEDLFFYSE--REANRSRDGAIVYCVGVD-FNE-TOLARI-----ADSKDHVP 121  
Db 260 DGQKFRDPLEYRHVYIPEAKA---GIRYALGVDAFREPALDELNTIGSAPSQDHVPK 316

QY 122 VNDGFOLQGIHSLKSCIEILAAEPSTICAGESFOVVVRGNGFPHARNVD 174  
Db 317 VGN-FVALRSIORQIOEK-----IFAIEGTESRSSSSFOHEMSQGFSSALSM 364

RESULT 3  
US-08-362-652-46  
; Sequence 46, Application US/08362652  
; Patent No. 5766850  
; GENERAL INFORMATION:  
; APPLICANT: Gallatin, W. Michael  
; APPLICANT: Van der Vlieten, Monica  
; TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit  
; NUMBER OF SEQUENCES: 93  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 South Wacker Drive, 6300 Sear Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/362.652  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/173,497  
; FILING DATE: 23-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/286,889  
; FILING DATE: 5-AUG-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams Jr., Joseph A.  
; REGISTRATION NUMBER: 38,659  
; REFERENCE/DOCKET NUMBER: 27866/32391  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; TELEFAX: 312-474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 46:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1155 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-362-652-46

Query Match 11.4%; Score 128.5; DB 1; Length 1155;  
Best Local Similarity 28.9%; Pred. No. 1.2e-05;  
Matches 50; Conservative 31; Mismatches 69; Indels 23; Gaps 9;  
QY 12 TLMKLTEDREQIRGLBELQKVLPGDPTVMHEGFRASEQIYYENRGYRTA-SVIALT 70  
Db 205 TEFKSSLSQSLVDIAIVQLQ-----GLTYTASGIQKVKELEFHSNGARKSAKKILIVIT 259  
QY 71 DGEIHEDLFFYSE--REANRSRDGAIVYCVGVD-FNE-TOLARI-----ADSKDHVP 121  
Db 260 DGQKFRDPLEYRHVYIPEAKA---GIRYALGVDAFREPALDELNTIGSAPSQDHVPK 316  
QY 122 VNDGFOLQGIHSLKSCIEILAAEPSTICAGESFOVVVRGNGFPHARNVD 174  
Db 317 VGN-FVALRSIORQIOEK-----IFAIEGTESRSSSSFOHEMSQGFSSALSM 364

RESULT 4  
US-08-605-672-46  
; Sequence 46, Application US/08605672  
; Patent No. 5817515

GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Sear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/605,672  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1155 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-605-672-46

Query Match 11.4%; Score 128.5; DB 2; Length 1155;  
Best Local Similarity 28.9%; Pred. No. 1.2e-05;  
Matches 50; Conservative 31; Mismatches 69; Indels 23; Gaps 9;

QY 12 TLMKLTEDREQRLQLEBLQKVLPGSDTYMEGFERASEQIYYENRQGRTA-SVITALT 70  
DB 205 TEFKSLSPQSLVDAIVQLQ-----GLTYTAGIQKVKVELFHSKNGARKSAKKILIVIT 259  
QY 71 DGEIHEDLFFYSE--REANRSDLGAIYVCVGD-FNE-TOLARI-----ADSKDHVP 121  
DB 260 DQQRDPLEFRHYIPEAKA---GIIRYALGVDAFEPFALQELNTIGSAPSDHVPK 316

QY 122 VNDGFQALQGIHSLIKKSCIEILAEPTICAGSPQVYVNGNFRHARNVD 174  
DB 317 VGN-FVALRSIQRLQLEK-----IFALIGTESRSSSSFGHEMSQEGFSALSMND 364

RESULT 5  
US-08-482-293A-46  
Sequence 46, Application US/08482293A  
Patent No. 5831029  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Sear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,293A  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1155 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-482-293A-46

Query Match 11.4%; Score 128.5; DB 2; Length 1155;  
Best Local Similarity 28.9%; Pred. No. 1.2e-05;  
Matches 50; Conservative 31; Mismatches 69; Indels 23; Gaps 9;

QY 12 TLMKLTEDREQRLQLEBLQKVLPGSDTYMEGFERASEQIYYENRQGRTA-SVITALT 70  
DB 205 TEFKSLSPQSLVDAIVQLQ-----GLTYTAGIQKVKVELFHSKNGARKSAKKILIVIT 259  
QY 71 DGEIHEDLFFYSE--REANRSDLGAIYVCVGD-FNE-TOLARI-----ADSKDHVP 121  
DB 260 DQQRDPLEFRHYIPEAKA---GIIRYALGVDAFEPFALQELNTIGSAPSDHVPK 316

QY 122 VNDGFQALQGIHSLIKKSCIEILAEPTICAGSPQVYVNGNFRHARNVD 174  
DB 317 VGN-FVALRSIQRLQLEK-----IFALIGTESRSSSSFGHEMSQEGFSALSMND 364

RESULT 6  
US-08-943-363-46  
Sequence 46, Application US/08943363  
Patent No. 5837478  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Sear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943.363
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173.497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286.889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362.652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-943-363-46

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Query Match 11.4%; Score 128.5; DB 2; Length 1155;
Best Local Similarity 28.9%; Pred. No. 1.2e-05;
Matches 50; Conservative 31; Mismatches 69; Indels 23; Gaps 9;

Qy 12 TLMKLTREDRQIQGLEELQKVLPGSDTYMHGFERASBOIYYENRCGYRTA-SVITALT 70
Db 205 TEFKSSLSFQSLVDATVQLQ-----GLTYTASGIQKVKELFHSKNGARSAKKILIVIT 259
Qy 71 DGEIHEDLFFYSE--REANRSRDGAIVYCVGYVD-FNE-TOLARI-----ADSKDHVFP 121
Db 260 DGQKFRDPLRYRHVIPAERKA---GIIRYALGVGDAREPTALQELNTISGAPSDHVF 316
Qy 122 VNDGFOALQGIHSLKSCIEILAAEPSTTCAGESFOVVVRNGGFRHARNVD 174
Db 317 VGN-FVALRSTIORQIOEK----IFAIEGTESRSSSFQHEMSQGFSSALSM 364

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RESULT 7
; US-09-193-043-46
; Sequence 46, Application US/09193043
; Patent No. 6251395
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; TITLE OF INVENTION: No. 6251395el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/193.043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173.497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286.889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362.652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943.363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 46

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; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-193-043-46

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Query Match 11.4%; Score 128.5; DB 3; Length 1155;
Best Local Similarity 28.9%; Pred. No. 1.2e-05;
Matches 50; Conservative 31; Mismatches 69; Indels 23; Gaps 9;

Qy 12 TLMKLTREDRQIQGLEELQKVLPGSDTYMHGFERASBOIYYENRCGYRTA-SVITALT 70
Db 205 TEFKSSLSFQSLVDATVQLQ-----GLTYTASGIQKVKELFHSKNGARSAKKILIVIT 259
Qy 71 DGEIHEDLFFYSE--REANRSRDGAIVYCVGYVD-FNE-TOLARI-----ADSKDHVFP 121
Db 260 DGQKFRDPLRYRHVIPAERKA---GIIRYALGVGDAREPTALQELNTISGAPSDHVF 316
Qy 122 VNDGFOALQGIHSLKSCIEILAAEPSTTCAGESFOVVVRNGGFRHARNVD 174
Db 317 VGN-FVALRSTIORQIOEK----IFAIEGTESRSSSFQHEMSQGFSSALSM 364

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RESULT 8
; US-09-688-307A-46
; Sequence 46, Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; TITLE OF INVENTION: No. 6432404el Human Beta-2
; FILE REFERENCE: 27866/36646
; CURRENT APPLICATION NUMBER: US/09/688.307A
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193.043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605.672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173.497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286.889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362.652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943.363
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 46
; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-688-307A-46

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Query Match 11.4%; Score 128.5; DB 4; Length 1155;
Best Local Similarity 28.9%; Pred. No. 1.2e-05;
Matches 50; Conservative 31; Mismatches 69; Indels 23; Gaps 9;

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Qy 12 TLMKLTREDRQIQGLEELQKVLPGSDTYMHGFERASBOIYYENRCGYRTA-SVITALT 70
Db 205 TEFKSSLSFQSLVDATVQLQ-----GLTYTASGIQKVKELFHSKNGARSAKKILIVIT 259
Qy 71 DGEIHEDLFFYSE--REANRSRDGAIVYCVGYVD-FNE-TOLARI-----ADSKDHVFP 121
Db 260 DGQKFRDPLRYRHVIPAERKA---GIIRYALGVGDAREPTALQELNTISGAPSDHVF 316
Qy 122 VNDGFOALQGIHSLKSCIEILAAEPSTTCAGESFOVVVRNGGFRHARNVD 174
Db 317 VGN-FVALRSTIORQIOEK----IFAIEGTESRSSSFQHEMSQGFSSALSM 364

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RESULT 9
; US-09-350-259-46
; Sequence 46, Application US/09350259

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Patent No. 6620915  
GENERAL INFORMATION:  
APPLICANT: Gallatin, Michael W.  
APPLICANT: Van der Vlieten, Monica  
TITLE OF INVENTION: No. 6620915el Human 2  
FILE REFERENCE: 27866/35004  
CURRENT APPLICATION NUMBER: US/09/350,259  
CURRENT FILING DATE: 1999-07-08  
EARLIER APPLICATION NUMBER: 09/193,043  
EARLIER FILING DATE: 1998-11-16  
EARLIER APPLICATION NUMBER: 08/173,497  
EARLIER FILING DATE: 1993-12-23  
EARLIER APPLICATION NUMBER: 08/286,889  
EARLIER FILING DATE: 1994-08-05  
EARLIER APPLICATION NUMBER: 08/362,652  
EARLIER FILING DATE: 1994-12-21  
EARLIER APPLICATION NUMBER: 08/943,363  
EARLIER FILING DATE: 1997-10-03  
NUMBER OF SEQ ID NOS: 114  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 46  
LENGTH: 1155  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-350-259-46

Query Match 11.4%, Score 128.5; DB 4; Length 1155;  
Best Local Similarity 28.9%, Pred. No. 1.2e-05;  
Matches 50; Conservative 31; Mismatches 69; Indels 23; Gaps 9;

Qy 12 TLMKLTEDREQIRQGLLELQKVLPGGDTYMHGFEFASQIYENRQGYRTA-SVITALT 70  
Db 205 TEFKSSLSPOSIVDAIVQLQ-----GLTYTASGIQKVKELFHSKNGARKSKAKILIVIT 259  
Qy 71 DGEIHEDLFYFSE--REANRSRDGAIVYCVGVD-FNE-TQLARI-----ADSKDHVP 121  
Db 260 DQKRPDLEVRHVIPEAKA---GIIRYAVGDAFREPALQELNLTIGSAPSGDHVFK 316  
Qy 122 VNDGFOALQGIITHSLKSCIEILAEPTTCAGSFQVVYVRGNGFRIRAVND 174  
Db 317 VGN-FVALRSIORQIOEK---IFAIBGTESRSSSFQHEMSQEGFSALSMD 364

RESULT 10  
US-08-485-618-53  
Sequence 53, Application US/08485618  
Patent No. 5728533  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
APPLICANT: Van der Vlieten, Monica  
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum  
STREET: 233 South Wacker Drive, 6300 Sear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,618  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32797  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1161 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-485-618-53

Query Match 11.4%, Score 128.5; DB 1; Length 1161;  
Best Local Similarity 28.9%, Pred. No. 1.2e-05;  
Matches 50; Conservative 31; Mismatches 69; Indels 23; Gaps 9;

Qy 12 TLMKLTEDREQIRQGLLELQKVLPGGDTYMHGFEFASQIYENRQGYRTA-SVITALT 70  
Db 205 TEFKSSLSPOSIVDAIVQLQ-----GLTYTASGIQKVKELFHSKNGARKSKAKILIVIT 259  
Qy 71 DGEIHEDLFYFSE--REANRSRDGAIVYCVGVD-FNE-TQLARI-----ADSKDHVP 121  
Db 260 DQKRPDLEVRHVIPEAKA---GIIRYAVGDAFREPALQELNLTIGSAPSGDHVFK 316  
Qy 122 VNDGFOALQGIITHSLKSCIEILAEPTTCAGSFQVVYVRGNGFRIRAVND 174  
Db 317 VGN-FVALRSIORQIOEK---IFAIBGTESRSSSFQHEMSQEGFSALSMD 364

RESULT 11  
US-08-362-652-53  
Sequence 53, Application US/08362652  
Patent No. 5766850  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
APPLICANT: Van der Vlieten, Monica  
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum  
STREET: 233 South Wacker Drive, 6300 Sear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,652  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32391  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1161 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-362-652-53

Query Match 11.4%; Score 128.5; DB 1; Length 1161;  
Best Local Similarity 28.9%; Pred. No. 1.2e-05;  
Matches 50; Conservative 31; Mismatches 69; Indels 23; Gaps 9;

Qy 12 TLMKLTEDRQIQGLBEIQKVLPGGDTYHMEGFERASQIYYENRQGRTA-SVITALT 70  
Db 205 TERKSSLSPOSIVDAIVQLQ-----GLTYTASGIQVVKELFHSKNGARKSAKKILIVIT 259  
Qy 71 DGEIHEDLPFYSE--REANRSRDIGAIVYCVGYKD-FNE-TOLARI-----ADSKDHVFP 121  
Db 260 DQGRFDPLRYRHVYIPEAKA---GIIRYAIQVGDAPREFPALQELNTIGSAPSQDHVFK 316  
Qy 122 VNDGFOLQGIHISILKSCIEIILAEPTICAGESFQVYVVRNGFRRHARNVD 174  
Db 317 VGN-FVALRSIORQIOEK----IFAIEGTESRSSSSFOHEMSQEGFSSALSMD 364

RESULT 12  
US-08-605-672-53  
Sequence 53, Application US/08605672  
Patent No. 5817515

GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Sear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/605,672  
FILING DATE:

CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:  
FILING DATE: 21-DEC-1994  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1161 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-605-672-53

Query Match 11.4%; Score 128.5; DB 2; Length 1161;  
Best Local Similarity 28.9%; Pred. No. 1.2e-05;  
Matches 50; Conservative 31; Mismatches 69; Indels 23; Gaps 9;

Qy 12 TLMKLTEDRQIQGLBEIQKVLPGGDTYHMEGFERASQIYYENRQGRTA-SVITALT 70  
Db 205 TERKSSLSPOSIVDAIVQLQ-----GLTYTASGIQVVKELFHSKNGARKSAKKILIVIT 259  
Qy 71 DGEIHEDLPFYSE--REANRSRDIGAIVYCVGYKD-FNE-TOLARI-----ADSKDHVFP 121  
Db 260 DQGRFDPLRYRHVYIPEAKA---GIIRYAIQVGDAPREFPALQELNTIGSAPSQDHVFK 316  
Qy 122 VNDGFOLQGIHISILKSCIEIILAEPTICAGESFQVYVVRNGFRRHARNVD 174  
Db 317 VGN-FVALRSIORQIOEK----IFAIEGTESRSSSSFOHEMSQEGFSSALSMD 364

RESULT 13  
US-08-482-293A-53  
Sequence 53, Application US/08482293A  
Patent No. 5831029

GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Sear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,293A  
FILING DATE:

CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:  
FILING DATE: 21-DEC-1994  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1161 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-482-293A-53

Query Match 11.4%; Score 128.5; DB 2; Length 1161;

Best Local Similarity 28.9%; Pred. No. 1.2e-05;  
Matches 50; Conservative 31; Mismatches 69; Indels 23; Gaps 9;

QY 12 TLMKLTEDREOIRQGLLEIQLKVLPGSDTYMHEGFERASQIYENRQGYRTA-SVITALT 70  
DB 205 TEFKSSLSPOSLVDIAIVQLQ-----GLTYTASGIQKVVELPHSKNGARKSAKKILIVIT 259

QY 71 DGEIHEDLFYSE--REANRSRDIGAIYVCVVKD-FNE-TOLARI-----ADSKDHVP 121  
DB 260 DQKRPDLPEYRHVHVPBEAKA---GIIRYALGVDAFREPTALQELNTIGSAPSDHVPK 316

QY 122 VNDGFQALOGIIHSILKSCIEILAEPTICAGESFQVYVVGNGFRHARNVD 174  
DB 317 VGN-FVALRSIORQIOEK-----IFALIEGTERSSSSSFQHEMSQEGFSALSMD 364

RESULT 14  
US-08-943-363-53  
Sequence 53, Application US/08943363  
Patent No. 5837478  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
APPLICANT: Van der Vieren, Monica  
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Seair Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,363  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 2766/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1161 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-943-363-53

Query Match 11.4%; Score 128.5; DB 2; Length 1161;  
Best Local Similarity 28.9%; Pred. No. 1.2e-05;  
Matches 50; Conservative 31; Mismatches 69; Indels 23; Gaps 9;

QY 12 TLMKLTEDREOIRQGLLEIQLKVLPGSDTYMHEGFERASQIYENRQGYRTA-SVITALT 70  
DB 205 TEFKSSLSPOSLVDIAIVQLQ-----GLTYTASGIQKVVELPHSKNGARKSAKKILIVIT 259

QY 71 DGEIHEDLFYSE--REANRSRDIGAIYVCVVKD-FNE-TOLARI-----ADSKDHVP 121  
DB 260 DQKRPDLPEYRHVHVPBEAKA---GIIRYALGVDAFREPTALQELNTIGSAPSDHVPK 316

QY 122 VNDGFQALOGIIHSILKSCIEILAEPTICAGESFQVYVVGNGFRHARNVD 174  
DB 317 VGN-FVALRSIORQIOEK-----IFALIEGTERSSSSSFQHEMSQEGFSALSMD 364

RESULT 15  
US-09-193-043-53  
Sequence 53, Application US/09193043  
Patent No. 6251395  
GENERAL INFORMATION:  
APPLICANT: Gallatin, Michael W.  
APPLICANT: Van der Vieren, Monica  
TITLE OF INVENTION: No. 6251395el Human 2  
FILE REFERENCE: 27866/35004  
CURRENT APPLICATION NUMBER: US/09/193,043  
FILING DATE: 1998-11-16  
EARLIER APPLICATION NUMBER: 08/173,497  
EARLIER FILING DATE: 1993-12-23  
EARLIER APPLICATION NUMBER: 08/286,889  
EARLIER FILING DATE: 1994-08-05  
EARLIER APPLICATION NUMBER: 08/362,652  
EARLIER FILING DATE: 1994-12-21  
EARLIER APPLICATION NUMBER: 08/943,363  
EARLIER FILING DATE: 1997-10-03  
NUMBER OF SEQ ID NOS: 114  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 53  
LENGTH: 1161  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-193-043-53

Query Match 11.4%; Score 128.5; DB 3; Length 1161;  
Best Local Similarity 28.9%; Pred. No. 1.2e-05;  
Matches 50; Conservative 31; Mismatches 69; Indels 23; Gaps 9;

QY 12 TLMKLTEDREOIRQGLLEIQLKVLPGSDTYMHEGFERASQIYENRQGYRTA-SVITALT 70  
DB 205 TEFKSSLSPOSLVDIAIVQLQ-----GLTYTASGIQKVVELPHSKNGARKSAKKILIVIT 259

QY 71 DGEIHEDLFYSE--REANRSRDIGAIYVCVVKD-FNE-TOLARI-----ADSKDHVP 121  
DB 260 DQKRPDLPEYRHVHVPBEAKA---GIIRYALGVDAFREPTALQELNTIGSAPSDHVPK 316

QY 122 VNDGFQALOGIIHSILKSCIEILAEPTICAGESFQVYVVGNGFRHARNVD 174  
DB 317 VGN-FVALRSIORQIOEK-----IFALIEGTERSSSSSFQHEMSQEGFSALSMD 364

Search completed: June 21, 2004, 13:46:37  
Job time: 9.23196 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 21, 2004, 13:44:26 ; Search time 21.7559 Seconds

(without alignments)  
2828.859 Million cell updates/sec

Title: US-09-970-076-10

Perfect score: 1131

Sequence: 1 MSFVFSRGTTLMLKLTEDR.....STSGFKGNHPCUPARPT 218

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
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- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
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- 14: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of residues predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	977.5	86.4	504	14	US-10-201-292-34
2	966	85.4	328	14	US-10-038-307-26
3	966	85.4	328	14	US-10-201-292-26
4	966	85.4	333	10	US-09-796-753-12
5	966	85.4	333	14	US-10-038-307-2
6	966	85.4	333	14	US-10-201-292-2
7	966	85.4	342	14	US-10-038-307-22
8	966	85.4	342	14	US-10-201-292-22
9	966	85.4	345	14	US-10-038-307-24
10	966	85.4	345	14	US-10-201-292-24
11	966	85.4	403	11	US-09-833-245-621
12	966	85.4	529	14	US-10-201-292-36
13	966	85.4	551	14	US-10-038-307-18
14	966	85.4	551	14	US-10-201-292-18
15	966	85.4	564	12	US-09-918-715-187

16	966	85.4	564	12	US-09-918-715-232	Sequence 232, App
17	966	85.4	564	14	US-10-038-307-20	Sequence 20, App1
18	966	85.4	564	14	US-10-201-292-20	Sequence 20, App1
19	966	85.4	564	14	US-10-301-822-199	Sequence 199, App
20	966	85.4	564	16	US-10-408-765A-1823	Sequence 1823, App
21	961	85.0	403	11	US-09-833-245-620	Sequence 620, App
22	960	84.9	562	12	US-09-918-715-194	Sequence 194, App
23	960	84.9	562	12	US-09-918-715-301	Sequence 301, App
24	945	83.6	534	14	US-10-038-307-12	Sequence 12, App1
25	945	83.6	534	14	US-10-201-292-12	Sequence 12, App1
26	945	83.6	543	14	US-10-038-307-10	Sequence 10, App1
27	945	83.6	543	14	US-10-038-307-14	Sequence 14, App1
28	945	83.6	543	14	US-10-038-307-16	Sequence 16, App1
29	945	83.6	543	14	US-10-201-292-10	Sequence 10, App1
30	945	83.6	543	14	US-10-201-292-14	Sequence 14, App1
31	945	83.6	543	14	US-10-201-292-16	Sequence 16, App1
32	877	77.5	479	14	US-10-201-292-32	Sequence 32, App1
33	767	67.8	460	14	US-10-201-292-28	Sequence 28, App1
34	757	66.9	460	14	US-10-201-292-30	Sequence 30, App1
35	704	62.2	538	13	US-10-047-542-99	Sequence 99, App1
36	506	44.7	245	15	US-10-094-749-2134	Sequence 2134, App
37	506	44.7	272	15	US-10-264-237-1574	Sequence 1574, App
38	506	44.7	488	10	US-09-796-753-52	Sequence 52, App1
39	506	44.7	488	14	US-10-038-307-6	Sequence 6, App1
40	506	44.7	488	14	US-10-201-292-6	Sequence 6, App1
41	506	44.7	488	14	US-10-368-087-16	Sequence 16, App1
42	506	44.7	488	15	US-10-104-047-2639	Sequence 2639, App
43	505	44.7	587	9	US-09-764-870-312	Sequence 312, App
44	505	44.7	587	11	US-09-764-875-968	Sequence 968, App
45	505	44.7	587	14	US-10-125-540-312	Sequence 312, App

#### ALIGNMENTS

RESULT 1  
US-10-201-292-34  
; Sequence 34, Application US/10201292  
; Publication No. US20030144193A1  
; GENERAL INFORMATION:  
; APPLICANT: James B. ROTHMAN  
; APPLICANT: Theresa L. O'KEEFE  
; APPLICANT: English OZKANAYAK  
; APPLICANT: Judith J. HEALEY  
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
; FILE REFERENCE: 7853-253-999  
; CURRENT APPLICATION NUMBER: US/10/201,292  
; CURRENT FILING DATE: 2003-02-14  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 34  
; LENGTH: 504  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-201-292-34

Query Match 86.4%; Score 977.5; DB 14; Length 504;  
Best Local Similarity 91.1%; Pred. No. 8.6e-100;  
Matches 194; Conservative 3; Mismatches 9; Indels 7; Gaps 1;

QY	1	MSFVFSRGTTLMLKLTEDRQIRGLQVLPFGDPTVMHGEFRASBOIYYENROXY 60
DB	80	MSFVFSRGTTLMLKLTEDRQIRGLQVLPFGDPTVMHGEFRASBOIYYENROXY 139
QY	61	RTASVYIALTQGLHEDLFYSEERANRSRDGAIYVCVGDVFNFTOLARLADSKDHF 120
DB	140	RTASVYIALTQGLHEDLFYSEERANRSRDGAIYVCVGDVFNFTOLARLADSKDHF 199
QY	121	PVNDFOALQGIHSHILKKSCEIILAAPSTICAGESQVYVRGNGFPHARVAVLCSF 180
DB	200	PVNDFOALQGIHSHILKKSCEIILAAPSTICAGESQVYVRGNGFPHARVAVLCSF 259
QY	181	KINDSVTLKSLQSPWVSTSGFKGNHPCUP 213

Db 260 KINDSVTLINEKPFSPKSSD-----KTHTCP 285

## RESULT 2

US-10-038-307-26  
Sequence 26, Application US/10038307  
Publication No. US20030134786A1  
GENERAL INFORMATION:  
APPLICANT: James B. ROTTMAN  
APPLICANT: Theresa L. O'KEEFE  
APPLICANT: Engin OZKANNAK  
APPLICANT: Judith J. HEALEY  
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
FILE REFERENCE: 7853-253-999  
CURRENT APPLICATION NUMBER: US/10/038,307  
CURRENT FILING DATE: 2002-06-28  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 26  
LENGTH: 328  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-038-307-26

Query Match 85.4%; Score 966; DB 14; Length 328;  
Best Local Similarity 98.9%; Pred. No. 8,6e-99;  
Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSFVFSRGTTLMLKLTEDREIQGLLELQKVLPGSDTYMHGFERASEQIYYENRQGY 60  
Db 80 MSFVFSRGTTLMLKLTEDREIQGLLELQKVLPGSDTYMHGFERASEQIYYENRQGY 139  
Qy 61 RTASVITALTGDELHEDLPFYSEREANSRDLGAIYVCVGKDPNETQLARIADSKDHF 120  
Db 140 RTASVITALTGDELHEDLPFYSEREANSRDLGAIYVCVGKDPNETQLARIADSKDHF 199  
Qy 121 PVDGFOALQGIHSHILKSCIEITLAEPSTICAGESFOVYVVRNGGFRHANVDRVLCSE 180  
Db 200 PVDGFOALQGIHSHILKSCIEITLAEPSTICAGESFOVYVVRNGGFRHANVDRVLCSE 259  
Qy 181 KINDSVTLSK 190  
Db 260 KINDSVTLINE 269

## RESULT 3

US-10-201-292-26  
Sequence 26, Application US/10201292  
Publication No. US20030144193A1  
GENERAL INFORMATION:  
APPLICANT: James B. ROTTMAN  
APPLICANT: Theresa L. O'KEEFE  
APPLICANT: Engin OZKANNAK  
APPLICANT: Judith J. HEALEY  
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
FILE REFERENCE: 7853-253-999  
CURRENT APPLICATION NUMBER: US/10/201,292  
CURRENT FILING DATE: 2003-02-14  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 26  
LENGTH: 328  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-201-292-26

Query Match 85.4%; Score 966; DB 14; Length 328;  
Best Local Similarity 98.9%; Pred. No. 8,6e-99;  
Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSFVFSRGTTLMLKLTEDREIQGLLELQKVLPGSDTYMHGFERASEQIYYENRQGY 60

Db 80 MSFVFSRGTTLMLKLTEDREIQGLLELQKVLPGSDTYMHGFERASEQIYYENRQGY 139  
Qy 61 RTASVITALTGDELHEDLPFYSEREANSRDLGAIYVCVGKDPNETQLARIADSKDHF 120  
Db 140 RTASVITALTGDELHEDLPFYSEREANSRDLGAIYVCVGKDPNETQLARIADSKDHF 199  
Qy 121 PVDGFOALQGIHSHILKSCIEITLAEPSTICAGESFOVYVVRNGGFRHANVDRVLCSE 180  
Db 200 PVDGFOALQGIHSHILKSCIEITLAEPSTICAGESFOVYVVRNGGFRHANVDRVLCSE 259  
Qy 181 KINDSVTLSK 190  
Db 260 KINDSVTLINE 269

## RESULT 4

US-09-796-753-12  
Sequence 12, Application US/09796753  
Publication No. US20030027998A1  
GENERAL INFORMATION:  
APPLICANT: McCarthy, Sean A.  
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF  
FILE REFERENCE: 7853-227-999  
CURRENT APPLICATION NUMBER: US/09/796,753  
CURRENT FILING DATE: 2001-03-01  
PRIOR APPLICATION NUMBER: 09/183,175  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: 09/223,094  
PRIOR FILING DATE: 1998-12-30  
PRIOR APPLICATION NUMBER: 09/223,546  
PRIOR FILING DATE: 1998-12-30  
PRIOR APPLICATION NUMBER: 09/224,246  
PRIOR FILING DATE: 1998-12-30  
PRIOR APPLICATION NUMBER: 09/259,388  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: 60/122,458  
PRIOR FILING DATE: 1999-03-01  
PRIOR APPLICATION NUMBER: 09/312,359  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 09/336,536  
PRIOR FILING DATE: 1999-06-18  
PRIOR APPLICATION NUMBER: 09/342,687  
PRIOR FILING DATE: 1999-06-29  
PRIOR APPLICATION NUMBER: 09/345,464  
PRIOR FILING DATE: 1999-06-30  
PRIOR APPLICATION NUMBER: 09/365,164  
PRIOR FILING DATE: 1999-07-30  
PRIOR APPLICATION NUMBER: 09/399,723  
PRIOR FILING DATE: 1999-09-20  
PRIOR APPLICATION NUMBER: 09/409,634  
PRIOR FILING DATE: 1999-09-30  
PRIOR APPLICATION NUMBER: 09/471,179  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 09/474,071  
PRIOR FILING DATE: 1999-12-29  
PRIOR APPLICATION NUMBER: 09/474,072  
PRIOR FILING DATE: 1999-12-29  
PRIOR APPLICATION NUMBER: 09/514,010  
PRIOR FILING DATE: 2000-02-25  
PRIOR APPLICATION NUMBER: 09/516,745  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: 09/572,002  
PRIOR FILING DATE: 2000-05-14  
PRIOR APPLICATION NUMBER: 09/597,993  
PRIOR FILING DATE: 2000-06-19  
PRIOR APPLICATION NUMBER: 09/599,596  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: 09/630,334  
PRIOR FILING DATE: 2000-07-31  
PRIOR APPLICATION NUMBER: 09/606,565  
PRIOR FILING DATE: 2000-06-29  
PRIOR APPLICATION NUMBER: 09/606,317  
PRIOR FILING DATE: 2000-06-29

PRIOR APPLICATION NUMBER: 09/665,666  
PRIOR FILING DATE: 2000-09-20  
PRIOR APPLICATION NUMBER: 09/677,751  
PRIOR FILING DATE: 2000-09-30  
NUMBER OF SEQ ID NOS: 162  
SEQ ID NO 12  
LENGTH: 333  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-796-753-12

Query Match 85.4%; Score 966; DB 10; Length 333;  
Best Local Similarity 98.9%; Pred. No. 8.8e-99;  
Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFVFSRGTTLMLKLTEDREQIRQGLEBQKVLPGGDTYMHGFERASEQIYYENRQGY 60  
DB 80 MSFVFSRGTTLMLKLTEDREQIRQGLEBQKVLPGGDTYMHGFERASEQIYYENRQGY 139  
QY 61 RTASVITALTGDELHEDLFFYSEREANRSRDIGALVYCVGVDPNETQIARIADSKDHF 120  
DB 140 RTASVITALTGDELHEDLFFYSEREANRSRDIGALVYCVGVDPNETQIARIADSKDHF 199  
QY 121 PVNDGFOALQGIHSLKSCIEILAEPSITCAGESFQVVRGNGFPHARVNDVLCSE 180  
DB 200 PVNDGFOALQGIHSLKSCIEILAEPSITCAGESFQVVRGNGFPHARVNDVLCSE 259  
QY 181 KINDSVTLSK 190  
DB 260 KINDSVTLINE 269

## RESULT 5

US-10-038-307-2  
Sequence 2, Application US/10038307  
Publication No. US20030134786A1  
GENERAL INFORMATION:  
APPLICANT: James B. ROTTMAN  
APPLICANT: Theresa L. O'KEEFE  
APPLICANT: Engin OZKAYNAK  
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
FILE REFERENCE: 7853-253-999  
CURRENT APPLICATION NUMBER: US/10/038,307  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 333  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-038-307-2

Query Match 85.4%; Score 966; DB 14; Length 333;  
Best Local Similarity 98.9%; Pred. No. 8.8e-99;  
Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFVFSRGTTLMLKLTEDREQIRQGLEBQKVLPGGDTYMHGFERASEQIYYENRQGY 60  
DB 80 MSFVFSRGTTLMLKLTEDREQIRQGLEBQKVLPGGDTYMHGFERASEQIYYENRQGY 139  
QY 61 RTASVITALTGDELHEDLFFYSEREANRSRDIGALVYCVGVDPNETQIARIADSKDHF 120  
DB 140 RTASVITALTGDELHEDLFFYSEREANRSRDIGALVYCVGVDPNETQIARIADSKDHF 199  
QY 121 PVNDGFOALQGIHSLKSCIEILAEPSITCAGESFQVVRGNGFPHARVNDVLCSE 180  
DB 200 PVNDGFOALQGIHSLKSCIEILAEPSITCAGESFQVVRGNGFPHARVNDVLCSE 259  
QY 181 KINDSVTLSK 190  
DB 260 KINDSVTLINE 269

## RESULT 6

US-10-201-292-2  
Sequence 2, Application US/10201292  
Publication No. US20030144193A1  
GENERAL INFORMATION:  
APPLICANT: James B. ROTTMAN  
APPLICANT: Theresa L. O'KEEFE  
APPLICANT: Engin OZKAYNAK  
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
FILE REFERENCE: 7853-253-999  
CURRENT APPLICATION NUMBER: US/10/201,292  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 333  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-201-292-2

Query Match 85.4%; Score 966; DB 14; Length 333;  
Best Local Similarity 98.9%; Pred. No. 8.8e-99;  
Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFVFSRGTTLMLKLTEDREQIRQGLEBQKVLPGGDTYMHGFERASEQIYYENRQGY 60  
DB 80 MSFVFSRGTTLMLKLTEDREQIRQGLEBQKVLPGGDTYMHGFERASEQIYYENRQGY 139  
QY 61 RTASVITALTGDELHEDLFFYSEREANRSRDIGALVYCVGVDPNETQIARIADSKDHF 120  
DB 140 RTASVITALTGDELHEDLFFYSEREANRSRDIGALVYCVGVDPNETQIARIADSKDHF 199  
QY 121 PVNDGFOALQGIHSLKSCIEILAEPSITCAGESFQVVRGNGFPHARVNDVLCSE 180  
DB 200 PVNDGFOALQGIHSLKSCIEILAEPSITCAGESFQVVRGNGFPHARVNDVLCSE 259  
QY 181 KINDSVTLSK 190  
DB 260 KINDSVTLINE 269

## RESULT 7

US-10-038-307-22  
Sequence 22, Application US/10038307  
Publication No. US20030134786A1  
GENERAL INFORMATION:  
APPLICANT: James B. ROTTMAN  
APPLICANT: Theresa L. O'KEEFE  
APPLICANT: Engin OZKAYNAK  
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
FILE REFERENCE: 7853-253-999  
CURRENT APPLICATION NUMBER: US/10/038,307  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 22  
LENGTH: 342  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-038-307-22

Query Match 85.4%; Score 966; DB 14; Length 342;  
Best Local Similarity 98.9%; Pred. No. 9.2e-99;  
Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFVFSRGTTLMLKLTEDREQIRQGLEBQKVLPGGDTYMHGFERASEQIYYENRQGY 60  
DB 89 MSFVFSRGTTLMLKLTEDREQIRQGLEBQKVLPGGDTYMHGFERASEQIYYENRQGY 148  
QY 61 RTASVITALTGDELHEDLFFYSEREANRSRDIGALVYCVGVDPNETQIARIADSKDHF 120

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Db      149 RTASVITLTDGELHEDLFFYSEREANSRDLGAIYVCVGDYVHGFERASEQIYYENRQGY 208
QY      121 PVNDGFQALOGIHSILKSCIEILAEPSITCAGESFQVYVVRNGGFRHARNVDRVLCSE 180
Db      209 PVNDGFQALOGIHSILKSCIEILAEPSITCAGESFQVYVVRNGGFRHARNVDRVLCSE 268
QY      181 KINDSVTLSK 190
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Db      269 KINDSVTLINE 278

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# RESULT 8

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; Sequence 22, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7653-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-201-292-22

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Query Match      85.4%; Score 966; DB 14; Length 342;
Best Local Similarity 98.9%; Pred. No. 9.2e-99;
Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGSDTYMHGFERASEQIYYENRQGY 60
Db      89 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGSDTYMHGFERASEQIYYENRQGY 148
QY      61 RTASVITLTDGELHEDLFFYSEREANSRDLGAIYVCVGDYVHGFERASEQIYYENRQGY 120
Db      149 RTASVITLTDGELHEDLFFYSEREANSRDLGAIYVCVGDYVHGFERASEQIYYENRQGY 208
QY      121 PVNDGFQALOGIHSILKSCIEILAEPSITCAGESFQVYVVRNGGFRHARNVDRVLCSE 180
Db      209 PVNDGFQALOGIHSILKSCIEILAEPSITCAGESFQVYVVRNGGFRHARNVDRVLCSE 268
QY      181 KINDSVTLSK 190
        |||||:
Db      269 KINDSVTLINE 278

```

# RESULT 9

```

; Sequence 24, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7653-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens

```

# US-10-038-307-24

```

Query Match      85.4%; Score 966; DB 14; Length 345;
Best Local Similarity 98.9%; Pred. No. 9.3e-99;
Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGSDTYMHGFERASEQIYYENRQGY 60
Db      80 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGSDTYMHGFERASEQIYYENRQGY 139
QY      61 RTASVITLTDGELHEDLFFYSEREANSRDLGAIYVCVGDYVHGFERASEQIYYENRQGY 120
Db      140 RTASVITLTDGELHEDLFFYSEREANSRDLGAIYVCVGDYVHGFERASEQIYYENRQGY 199
QY      121 PVNDGFQALOGIHSILKSCIEILAEPSITCAGESFQVYVVRNGGFRHARNVDRVLCSE 180
Db      200 PVNDGFQALOGIHSILKSCIEILAEPSITCAGESFQVYVVRNGGFRHARNVDRVLCSE 259
QY      181 KINDSVTLSK 190
        |||||:
Db      260 KINDSVTLINE 269

```

# RESULT 10

```

; Sequence 24, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7653-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-201-292-24

```

```

Query Match      85.4%; Score 966; DB 14; Length 345;
Best Local Similarity 98.9%; Pred. No. 9.3e-99;
Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGSDTYMHGFERASEQIYYENRQGY 60
Db      80 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGSDTYMHGFERASEQIYYENRQGY 139
QY      61 RTASVITLTDGELHEDLFFYSEREANSRDLGAIYVCVGDYVHGFERASEQIYYENRQGY 120
Db      140 RTASVITLTDGELHEDLFFYSEREANSRDLGAIYVCVGDYVHGFERASEQIYYENRQGY 199
QY      121 PVNDGFQALOGIHSILKSCIEILAEPSITCAGESFQVYVVRNGGFRHARNVDRVLCSE 180
Db      200 PVNDGFQALOGIHSILKSCIEILAEPSITCAGESFQVYVVRNGGFRHARNVDRVLCSE 259
QY      181 KINDSVTLSK 190
        |||||:
Db      260 KINDSVTLINE 269

```

# RESULT 11

```

; Sequence 621, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: P546PCT

```



```

; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 621
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-621

Query Match      85.4%; Score 966; DB 11; Length 403;
Best Local Similarity 98.9%; Pred. No. 1.2e-98;
Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFVFSRGTTLMLKLTEDREIQRLQLELQVLPFGDTVMHEGPERASEQIYYENRQGY 60
DB 80 MSFVFSRGTTLMLKLTEDREIQRLQLELQVLPFGDTVMHEGPERASEQIYYENRQGY 139
QY 61 RTASVITLTDGELHEDLFFYSEREANRSRDGAIIVYCVGVKDFNETOLARIADSKDHF 120
DB 140 RTASVITLTDGELHEDLFFYSEREANRSRDGAIIVYCVGVKDFNETOLARIADSKDHF 199
QY 121 PVNDGFQALQGIHISILKKSCEIILAEPSITCAGESFQVVRVNGGPFHARVNDVRLCSF 180
DB 200 PVNDGFQALQGIHISILKKSCEIILAEPSITCAGESFQVVRVNGGPFHARVNDVRLCSF 259
QY 181 KINDSVTLTK 190
DB 260 KINDSVTLTK 269

RESULT 12
US-10-201-292-36
; Sequence 36, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Engin OZKANNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 36
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-36

Query Match      85.4%; Score 966; DB 14; Length 529;
Best Local Similarity 98.9%; Pred. No. 1.8e-98;
Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFVFSRGTTLMLKLTEDREIQRLQLELQVLPFGDTVMHEGPERASEQIYYENRQGY 60
DB 80 MSFVFSRGTTLMLKLTEDREIQRLQLELQVLPFGDTVMHEGPERASEQIYYENRQGY 139
QY 61 RTASVITLTDGELHEDLFFYSEREANRSRDGAIIVYCVGVKDFNETOLARIADSKDHF 120
DB 140 RTASVITLTDGELHEDLFFYSEREANRSRDGAIIVYCVGVKDFNETOLARIADSKDHF 199
QY 121 PVNDGFQALQGIHISILKKSCEIILAEPSITCAGESFQVVRVNGGPFHARVNDVRLCSF 180
DB 200 PVNDGFQALQGIHISILKKSCEIILAEPSITCAGESFQVVRVNGGPFHARVNDVRLCSF 259
QY 181 KINDSVTLTK 190
DB 260 KINDSVTLTK 269
```

```

QY 181 KINDSVTLTK 190
DB 260 KINDSVTLTK 269

RESULT 13
US-10-038-307-18
; Sequence 18, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Engin OZKANNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 18
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-18

Query Match      85.4%; Score 966; DB 14; Length 551;
Best Local Similarity 98.9%; Pred. No. 1.9e-98;
Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFVFSRGTTLMLKLTEDREIQRLQLELQVLPFGDTVMHEGPERASEQIYYENRQGY 60
DB 80 MSFVFSRGTTLMLKLTEDREIQRLQLELQVLPFGDTVMHEGPERASEQIYYENRQGY 139
QY 61 RTASVITLTDGELHEDLFFYSEREANRSRDGAIIVYCVGVKDFNETOLARIADSKDHF 120
DB 140 RTASVITLTDGELHEDLFFYSEREANRSRDGAIIVYCVGVKDFNETOLARIADSKDHF 199
QY 121 PVNDGFQALQGIHISILKKSCEIILAEPSITCAGESFQVVRVNGGPFHARVNDVRLCSF 180
DB 200 PVNDGFQALQGIHISILKKSCEIILAEPSITCAGESFQVVRVNGGPFHARVNDVRLCSF 259
QY 181 KINDSVTLTK 190
DB 260 KINDSVTLTK 269

RESULT 14
US-10-201-292-18
; Sequence 18, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Engin OZKANNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 18
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-18

Query Match      85.4%; Score 966; DB 14; Length 551;
Best Local Similarity 98.9%; Pred. No. 1.9e-98;
Matches 188; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

Qy	MSIVSTRCTTLMKLTEDREQLROGLLEQVLEGGGTYHHEGGERASEDIYENKQY 60
Db	MSIVSTRCTTLMKLTEDREQLROGLLEQVLEGGGTYHHEGGERASEDIYENKQY 139
Qy	RTASVLIATDGLHEDLFFYSERENRSGDIALVYCVGKDFNETOLARIADSKDHF 120
Db	RTASVLIATDGLHEDLFFYSERENRSGDIALVYCVGKDFNETOLARIADSKDHF 199
Qy	PVNDGFOALGGIIHSILKKSCEIILAESTICAGESQVYVYRNGRFRHNRDVLCSF 180
Db	PVNDGFOALGGIIHSILKKSCEIILAESTICAGESQVYVYRNGRFRHNRDVLCSF 259
Qy	KINDSVTLK 190
Db	KINDSVTLNE 269

```

RESULT 15
US-09-918-715-187
; Sequence 187, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918, 715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-187

```

Query Match	85.4%	Score 966	DB 12	Length 564
Best Local Similarity	98.9%	Pred. No. 1.9e-98		
Matches 188	Conservative	2	Mismatches 0	Indels 0
			Gaps	0

QY MSFVFESTRGTTLMKLTLEBEOIROLLELOKVLGSGPTVMEGPERASEDITYENKQY 60  
Db MSFVSVSTRGTTLMKLTLEBEOIROLLELOKVLGSGPTVMEGPERASEDITYENKQY 139  
QY 61 RTASVIALTDGELHEDLPFYSERENRSDIGAIVYCVGYD FNETOLARIADSKHVF 120  
Db 140 RTASVIALTDGELHEDLPFYSERENRSDIGAIVYCVGYD FNETOLARIADSKHVF 139  
QY 121 PVNDGFALOGIIHSLIKKSCIEIILAEPSTI CAGESFQVYVVRNGGFHANVDVILCSF 180  
Db 200 PVNDGFALOGIIHSLIKKSCIEIILAEPSTI CAGESFQVYVVRNGGFHANVDVILCSF 259  
QY 181 KINDSVTLSK 190  
Db 260 KINDSVTLINE 269

Search completed: June 21, 2004, 14:02:14  
Job time : 21.7559 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 22, 2004, 02:37:46 ; Search time 496.02 Seconds  
(without alignments)  
3075.489 Million cell updates/sec

Title: US-09-970-076-8  
Perfect score: 1728  
Sequence: 1 MATERNALGIGFOWLSIAT.....TTHCSLHKAIGPTTAACME 333

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3017426 seqs, 2290544650 residues  
Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+ p2n.model -DEV=xlh  
-O=/cgn2\_1/USPTO.apool/US09970076/runac\_21062004\_125533\_8805/app.query.fasta\_1.2140  
-DB=Published Applications NA -QMT=fastcap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPT=0 -LOOPTXT=0 -UNITs=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US09970076 @CEN 1.1 1225 @runac\_21062004\_125533\_8805  
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -TRENDS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
Published Applications NA:  
1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/PCTOS\_PUBCOMB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
------------	-------	-------	-------	--------	-------	-------------

1	1728	100.0	1713	15	US-10-038-307-19	Sequence 19, Appl
2	1728	100.0	1713	15	US-10-201-292-19	Sequence 19, Appl
3	1728	100.0	2272	15	US-09-796-753-11	Sequence 11, Appl
4	1728	100.0	2272	15	US-10-038-307-1	Sequence 1, Appl1
5	1728	100.0	2272	15	US-10-201-292-1	Sequence 1, Appl1
6	1728	100.0	2353	15	US-10-198-846-9957	Sequence 9957, Ap
7	1728	100.0	2459	9	US-09-833-381-998	Sequence 998, App
8	1718	99.4	1056	15	US-10-038-307-23	Sequence 23, Appl
9	1718	99.4	1056	15	US-10-201-292-23	Sequence 23, Appl
10	1713.5	99.2	1047	15	US-10-038-307-21	Sequence 21, Appl
11	1713.5	99.2	1047	15	US-10-201-292-21	Sequence 21, Appl
12	1650.5	95.5	1674	15	US-10-038-307-17	Sequence 17, Appl
13	1650.5	95.5	1674	15	US-10-201-292-17	Sequence 17, Appl
14	1649	95.4	1454	16	US-10-133-537-58	Sequence 58, Appl
15	1649	95.4	1454	16	US-10-159-653-58	Sequence 58, Appl
16	1649	95.4	1650	15	US-10-038-307-13	Sequence 13, Appl
17	1649	95.4	1650	15	US-10-038-307-15	Sequence 15, Appl
18	1649	95.4	1650	15	US-10-201-292-13	Sequence 13, Appl
19	1649	95.4	1650	15	US-10-201-292-15	Sequence 15, Appl
20	1649	95.4	5540	13	US-09-918-715-176	Sequence 176, App
21	1649	95.4	5540	13	US-09-918-715-231	Sequence 231, App
22	1649	95.4	5540	15	US-10-301-822-198	Sequence 198, App
23	1639	94.8	1650	15	US-10-038-307-9	Sequence 9, Appl1
24	1639	94.8	1650	15	US-10-201-292-9	Sequence 9, Appl1
25	1636	94.7	1008	15	US-10-038-307-25	Sequence 25, Appl
26	1636	94.7	1008	15	US-10-201-292-25	Sequence 25, Appl
27	1599	92.5	2397	16	US-10-062-674-1757	Sequence 1757, Ap
28	1556	90.0	1608	15	US-10-201-292-35	Sequence 35, Appl
29	1553	89.9	5220	13	US-09-918-715-186	Sequence 186, App
30	1553	89.9	5220	13	US-09-918-715-300	Sequence 300, App
31	1508	87.3	1623	15	US-10-038-307-11	Sequence 11, Appl
32	1508	87.3	1623	15	US-10-201-292-11	Sequence 11, Appl
33	1423	82.3	1534	15	US-10-201-292-33	Sequence 33, Appl
34	1392	80.6	1609	15	US-10-037-270-8	Sequence 8, Appl1
35	1392	80.6	1609	16	US-10-117-122-8	Sequence 8, Appl1
36	1313	76.0	1464	15	US-10-201-292-31	Sequence 31, Appl
37	1193	69.0	1401	15	US-10-201-292-27	Sequence 27, Appl
38	1193	69.0	1401	15	US-10-201-292-27	Sequence 27, Appl
39	903	52.3	1650	14	US-10-047-542-98	Sequence 98, Appl
40	903	52.3	6602	14	US-10-047-542-100	Sequence 100, App
41	800.5	46.3	2234	16	US-10-104-047-669	Sequence 669, App
42	800.5	46.3	3677	10	US-09-796-753-51	Sequence 51, Appl
43	800.5	46.3	3677	15	US-10-038-307-5	Sequence 5, Appl
44	800.5	46.3	3677	15	US-10-201-292-5	Sequence 5, Appl
45	800.5	46.3	4081	15	US-10-368-087-9	Sequence 9, Appl1

## ALIGNMENTS

RESULT 1  
US-10-038-307-19  
; Sequence 19, Application US/10038307  
; Publication No. US20030134786A1  
GENERAL INFORMATION:  
APPLICANT: James B. ROTHMAN  
APPLICANT: Theresa L. O'KEEFE  
APPLICANT: Engin OKAYNAK  
APPLICANT: Judith J. HEALEY  
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
FILE REFERENCE: 7853-253-999  
CURRENT APPLICATION NUMBER: US/10/038,307  
CURRENT FILING DATE: 2002-06-28  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 19  
LENGTH: 1713  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-038-307-19  
Alignment Scores: 7.08e-220 Length: 1713  
Pred. No.: 1713

Score:	1728.00	Matches:	333
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	15	Gaps:	0

US-09-970-076-8 (1-333) x US-10-038-307-19 (1-1713)

QY	MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr	20
Db	13 ATGGCACGGCGAGCGAGAGGCCCTCGGCATCGGCTTCAGTGGCACT	72
QY	21 LeuValIleuIleCysAlaGlyGlnGlyArgArgIuAspGlyProAlaCysTyr	40
Db	73 CTGGTGCTCATTCGGCCGGCGAGAGGAGACCGACGAGAGATGGGGGCTCCAGCTGGTAC	122
QY	41 GlyGlyPheAspLeuTyrPheIleLeuAspIleSerGlySerValIleuHisIleTrpAsn	60
Db	133 GGGGGATTTCACCTGATCTTCATTGGACAATACGAAAGTGTGCTGCACACTGGAAAT	192
QY	61 GluIleTyrTyrPheValGluGlnIleuAlaHisIleuPheIleSerProGlnIleuArgMet	80
Db	193 GAATCTATTACTTGTGGACAGTTGGCTGCACAAATTCATCGCCACCACTTGAATG	252
QY	81 SerPheIleValPheSerThrArgGlyThrThrLeuMetIleuLeuThrGluAspArgGlu	100
Db	253 TCTCTTATGTCTTCTCCACCGGAGGACACCTTATGAACTGACAGAGACAGAGAA	312
QY	101 GlnIleArgGlnIleuGluGluLeuGlnIleuValLeuProGlyGlyAspThrTyrMet	120
Db	313 CAATCCGTCMAAGCCTTAGAAGAACTCCAGAAAGTTCGCCAGAGAGAGACACTTAATG	372
QY	121 HisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnIleTyrArg	140
Db	373 CATGAAAGATTGAAAGGCGCACTGACAGATTATTATGAAACAGACAGGTTACAG	432
QY	141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPheTyr	160
Db	433 ACAGCCAGCTCATCTTCATTGCTTGAATGAGAACTCCATGAAGATCTCTTTTCTAT	492
QY	161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal	180
Db	493 TCGAGAGGGAGGCTAATAGTGTCCAGATCTTGGCAATGTTTACTGTGGTGGGTG	552
QY	181 LysAspPheAsnGluThrGlnIleuAlaArgIleAlaAspSerLysAspHisValPhePro	200
Db	553 AAAGATTTCAATAGACACACAGCTGGCCCGGATTGGCGACAGTAAAGATCATGTGTCCC	612
QY	201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysValSerCys	220
Db	613 GTGAATGACGGCTTTCAGGCTCGCAGAGCATCATCTCAATTTTGAAAGATCTCTGC	672
QY	221 IleGluIleIleuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnValVal	240
Db	673 ATGCAAAATTTCACACTGAAACATTCACCAATATGTGACAGAGATCATTTTCAAGTGTCT	732
QY	241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValIleuCysSerPheLys	260
Db	733 GTGAGAGGAACGGCTTCCGACATGCCCGCAACGTGCACAGGCTCTCTGCAGCTTCAAG	792
QY	261 IleAsnAspSerValThrLeuAsnGluIleuProPheSerValGluAspThrTyrLeuIleu	280
Db	793 ATCAATGACTCGGCTCACACTCAATGAGAGCCCTTTTCTGTGAGAAATCACTTATTTACTG	852
QY	281 CysProAlaProIleIleuLysGluValGlyMetLysValAlaIleuGlnValSerMetAsn	300
Db	853 TGTCCAGCGCTATCTTAAAGAAAGTGGCAAGAAAGCTGCACCTCCAGCTCAGCATGAC	912
QY	301 AspGlyLeuSerPheIleSerSerSerValIleIleIleThrThrHisCysSerLeuHis	320
Db	913 GATGGCTCTCTTTATCTCCAGTGTGTGCATCATCACACACACACACTGAGCTTCAC	972
QY	321 LysIleAlaSerGlyProThrThrAlaAlaCysMetGlu	333

Db 973 AAAATGCATCAGGCCCCACACACAGCTGCTGCATGGA 1011

## RESULT 2

US-10-201-292-19  
; Sequence 19, Application US/10201292  
Publication No. US20020141020

; GENERAL INFORMATION:

APPLICANT: James B. ROYMAN  
APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK  
APPLICANT: Judith J. HEALEY

1 ; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
2  
3 ; FILER REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/201,292

; CURRENT FILING DATE: 2003-02-14  
 ; NUMBER OF SEQ ID NOS: 36

```
! SOFTWARE: FastSEQ for Windows Version 4.0.0
: SEO ID NO 19
```

LENGTH: 1713  
TYPE: DNA

ORGANISM: Homo sapiens

US-10-201-292-19

**Alignment Scores**  
**Pred. No.:**

Score: \_\_\_\_\_  
Percent Similar: \_\_\_\_\_

Best Local Similarity

```

query match:
DB:

```

US-09-970-076-8 (1-333) x US-10-201-292-19 (1-1713)

1 MotA]aThra]aC]uArC]a]a]a]v]a]a]v]b]a]a]n]T]m]a]u]S]e]r]a]a]a]Thr 20

[illegible]

13 ATGGCCACGCGCGAGCGGAGAGCCCTCGGCATCGGCTTCAGAGGCTCTCTTGGCCACT / 20

21 LeuValLeuIleCybAlaGlyGlnGlyValArgArgIuAbpGlyGlyProAlaCysIyr 400

Db 73 CTGGTCTCATCTGCGCCGGGCAAGGGGAGCGACGAGGAGGATGGGGGTCCAGCCTGTAC 13

41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValIleuHisIleTrpAsn 60

Db 133 GCGGATTGACCTGACTTCATTTGGACAATCAGAAGTGTGCTGCACCACTGGAT 199

61 GluLeuTyrTyrPheValGluGluLeuAlaHisIleValPheIleSerProGluLeuArgMet 80

1 9 3 2 5

[illegible]

81 serphenlevalphaserinrargglyinrtrvneumetcyaleutnrgslwabpgrcu 10

Db 253 TCCTTATTGTTTCTCCACCCGAGGAACAACCTTAATGAACTGACAGAAGACAGAGA 31

101 GlnIleArgGlnGlyLeuGluGluGluLeuGlnIleValLeuProGlyGlyAspThrTyrMet 12

Db 313 CAAATCGTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATG 37

QY 121 HisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnIleY TyrArg 14

Db 373 CATGAAGATTGMAAGGCCAGTGACGATTTATTATGMAACAGACAAGGGTACGG 43

**141** **EbnjaJagewoIrlat]ab]alawEbnjaenC]inC]urauH;acC]uabawEubphobothur** 16

[illegible]

DB 433 ACAGCCAGCGTCAATGCTTGACTGATGAGACCTCCATGAGATCTCTTTTCTAT 49

161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180

Db 493 TCAGAGAGGAGCTAATAGTCTCGAGATCTGGTGCAATTGTTACTGTGTTGGTGTG 55

181 LysAspPheAsnGluThrGlnLeuIaArgIleAAspSerLysAspHisValPhePro 20

Db 553 AAAGATTTCATGAGACACAGCTGGCCCGGATTGGCGACAGTAAGATCATGTGTTTCCC 611

QY 201 ValaenagpGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220  
 DB 613 GTGAATGAGCGCTTTCAGGCTCTGAGGCACTCATCTCAATTTGAAAGAGCTCTGC 672  
 QY 221 IleguileleuAlaAlaGluProSerThrIleCysAlaGlyLysPheGlnValAla 240  
 DB 673 ATCGAATTTCTAGAGCTGACCACTCCATCCATATGCGAGAGATCTTAATTTGTC 732  
 QY 241 ValaagGlyAenGlyPheArgHisAlaArgenValaAspArgValLeuCysSerPheLys 260  
 DB 733 GTGAAGAGAAACGGCTTCCGACATGCCCGCAACGTGACAGGCTCTGCGCTTCAAG 792  
 QY 261 IleaenapSerValThrLeuAenGlyLysPhePheSerValGluAspThrThrLeuLeu 280  
 DB 793 ATCAATGACTCGGTCACTCATATGAGAAAGCCCTTTCTGTGGAAGATCTTAATTACG 852  
 QY 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300  
 DB 853 TGTCCAGGCGCTATCTTAAAGAGTTGGCATGAAGCTGCATCCAGCTCAGCTGAAAC 912  
 QY 301 AapGlyLysSerPheIleSerSerSerValIleIleThrThrThrHisCysSerLeuHis 320  
 DB 913 GATGCGCTCTCTTTATCTCCAGTTCTGTCACTCATCACACACACAGTGTAGCTTCAC 972  
 QY 321 LysIleAlaSerGlyProThrThrAlaAlaCysMetGlu 333  
 DB 973 AAAATTGATCAGGCCCCACACAGCTGCTGATGAA 1011

# RESULT 3

US-09-796-753-11

Sequence 11, Application US/09796753

Publication No. US20030027998A1

GENERAL INFORMATION:

APPLICANT: McCarthy, Sean A.

TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF

FILE REFERENCE: 7853-227-999

CURRENT APPLICATION NUMBER: US/09/796,753

PRIOR APPLICATION NUMBER: 09/183,175

PRIOR FILING DATE: 1998-10-30

PRIOR APPLICATION NUMBER: 09/223,094

PRIOR FILING DATE: 1998-12-30

PRIOR APPLICATION NUMBER: 09/223,546

PRIOR FILING DATE: 1998-12-30

PRIOR APPLICATION NUMBER: 09/224,246

PRIOR FILING DATE: 1998-12-30

PRIOR APPLICATION NUMBER: 09/259,388

PRIOR FILING DATE: 1999-02-26

PRIOR APPLICATION NUMBER: 60/122,458

PRIOR FILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: 09/312,359

PRIOR FILING DATE: 1999-05-14

PRIOR APPLICATION NUMBER: 09/336,536

PRIOR FILING DATE: 1999-06-18

PRIOR APPLICATION NUMBER: 09/342,687

PRIOR FILING DATE: 1999-06-29

PRIOR APPLICATION NUMBER: 09/345,464

PRIOR FILING DATE: 1999-06-30

PRIOR APPLICATION NUMBER: 09/365,164

PRIOR FILING DATE: 1999-07-30

PRIOR APPLICATION NUMBER: 09/399,723

PRIOR FILING DATE: 1999-09-20

PRIOR APPLICATION NUMBER: 09/409,634

PRIOR FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: 09/471,179

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: 09/474,071

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: 09/474,072

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: 09/514,010

PRIOR FILING DATE: 2000-02-25

PRIOR APPLICATION NUMBER: 09/516,745  
 PRIOR FILING DATE: 2000-03-01  
 PRIOR APPLICATION NUMBER: 09/572,002  
 PRIOR FILING DATE: 2000-05-14  
 PRIOR APPLICATION NUMBER: 09/597,993  
 PRIOR FILING DATE: 2000-06-19  
 PRIOR APPLICATION NUMBER: 09/599,596  
 PRIOR FILING DATE: 2000-06-22  
 PRIOR APPLICATION NUMBER: 09/630,334  
 PRIOR FILING DATE: 2000-07-31  
 PRIOR APPLICATION NUMBER: 09/606,565  
 PRIOR FILING DATE: 2000-06-29  
 PRIOR APPLICATION NUMBER: 09/606,317  
 PRIOR FILING DATE: 2000-06-29  
 PRIOR APPLICATION NUMBER: 09/665,666  
 PRIOR FILING DATE: 2000-09-20  
 PRIOR APPLICATION NUMBER: 09/677,751  
 PRIOR FILING DATE: 2000-09-30  
 NUMBER OF SEQ ID NOS: 162  
 SEQ ID NO 11  
 LENGTH: 2272  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (213)...(1211)  
 US-09-796-753-11

## Alignment Scores:

Pred. No.: 1,13e-219 Length: 2272  
 Score: 1728.00 Matches: 333  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 10 Gaps: 0

US-09-970-076-8 (1-333) x US-09-796-753-11 (1-2272)

QY 1 MetaIaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnThrProLeuSerLeuAlaThr 20  
 DB 213 ATGGCCAGCGGAGCGGAGAGCCCTCGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT 272  
 QY 21 LeuValLeuIleCysAlaGlyGlnGlyIleArgArgGluAspGlyGlyProAlaCysTyr 40  
 DB 273 CTGGTCTCATCTGCGCGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 332  
 QY 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisHisIleTrpAsn 60  
 DB 333 GCGGATTTGACCTGTACTTATTGGAACAATCAGGAAGTGTCTGCACCACTGGAAAT 392  
 QY 61 GluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80  
 DB 393 GAATCTATTACTTTGTGGAACAGTGGCTCAACAATTCATCAGCCACAGTTGGAATG 452  
 QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100  
 DB 453 TCTTTATTGTTTCTTCCACCGAGGAACAACCTTAATGAACCTAAGAGACAGAGAA 512  
 QY 101 GlnIleArgGlnGlyLeuGluGluLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120  
 DB 513 CAATCCCTCAAGGCTGAGGAAGTCTCCAGAAAGTTCGCCAGAGGAGACACTTACATG 572  
 QY 121 HisGlyLysPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140  
 DB 573 CATGAAGATTTGAAAGGCGCGAGTACAGAGATTTTATGAAACAGACAGAGGATACAGG 632  
 QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyr 160  
 DB 633 ACAGCCAGGTCATCATTTGCTTGACTGAGAGACTCCATGAAGATCTTTTTCAT 692  
 QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180  
 DB 693 TCAGAGAGGAGGCTTAATAGGTCTGAGATCTGTGCAATTGTTACTGTGTGTGTG 752

Qy 181 LysaapPheAengluThrglnLeuAlaarglIleAlaapSerLyAspPhIvalPhePro 200  
Db 753 AAAAGTTTCATGAGACACAGCTGGCCGGATGTGGACAGTAAGGATCATGTGTTCCC 812  
Qy 201 ValaenapGlyPheGlnAlaLeuGlnGlyIleIleHiserIleuLylasSerCys 220  
Db 813 GTGATATGACGGCTTTCAGGCTCTCGACAGCATCATCAATTTTGAGAGAGCTTGC 872  
Qy 221 IleguileuAlaAlaGluProSerThrIleCysAlaGlyIleuSerPheGlnValVal 240  
Db 873 ATCGAATATCTAGCAGCTGAACCATCCACCATATGTGAGAGAGTCAATTCAGATTGC 932  
Qy 241 ValargGlyAenglyPheargHisAlaargAsnValaapArgValIleuCySerPheLys 260  
Db 933 GTGAGAGGAAGAGGCTTCGACATGCCGCAACGTGACAGGCTCTTCGACGCTTCAG 992  
Qy 261 IleAenapSerValThrleuAenglyLylasProPheSerValGluAepThrTytleuLeu 280  
Db 993 ATCAATGACTCGGTACACTCAATAGAGAGCCCTTTCTGTGAAAGATTAATTTACTG 1052  
Qy 281 CysProAlaProIleleuLylasGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300  
Db 1053 TGTCCAGCGCTTATCTTAAAGAGTTGACATGAAGCTGCACCTCCAGGTACAGTGAAC 1112  
Qy 301 AapGlyLeuSerPheIleSerSerSerValIleIleThrThrThHisCySerLeuHis 320  
Db 1113 GATGCCCTCTCTTTATCTCCAGTTCTGTGATCATCATCACACACACACTGTAGCTTCAC 1172  
Qy 321 LysIleAlaSerGlyProThrThrAlaAlaCyMetGlu 333  
Db 1173 AAAATTGCATCAGGCCCAACACAGCTGTGCATGAGAA 1211

RESULT 4  
US-10-038-307-1  
; Sequence 1, Application US/10038307  
; Publication No. US20030134786A1  
; GENERAL INFORMATION:  
; APPLICANT: James B. ROTTMAN  
; APPLICANT: Theresa L. O'KEEFE  
; APPLICANT: Engin OZKANNAK  
; APPLICANT: Judith J. HEALEY  
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
; FILE REFERENCE: 7853-253-999  
; CURRENT APPLICATION NUMBER: US/10/038,307  
; CURRENT FILING DATE: 2002-06-28  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2272  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (213) ... (1211)  
US-10-038-307-1

Alignment Scores:  
Pred. No.: 1,13e-219 Length: 2272  
Score: 1728.00 Matches: 333  
Percent Similarity: 100.00% Conservative: 333  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 15 Gaps: 0

US-09-970-076-8 (1-333) x US-10-038-307-1 (1-2272)

Qy 1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerIleuAlaThr 20  
Db 213 ATGGCAGCGCGGAGAGGAGGCTTCGGCATCGGCTTCAGTGGCTCTCTTGGCCACT 272  
Qy 21 LeuValIleuLylasGlyGlnGlyArgArgGluAapGlyGlyProAlaCySerTy 40

Db 273 CTGGTGTCTATCTGGCCGGGCAAGGGGAGCGAGGAGATGGGGGTCCAGCTGCTAC 332  
Qy 41 GlyIylPheAapLeuTyThrPheIleLeuAapLysSerGlySerValIleuHisIleTrpAsn 60  
Db 333 GCGCGATTATACCTGTACTTTCATTTTGACAAATCAGGAAGTGTGTGCACACTGGAAAT 392  
Qy 61 GluIleTyTyThrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80  
Db 393 GAATCTATTAATCTTGTGGAACAGTTGGCTCACAAATTCATCAGCCACAGTTGAGAAATG 452  
Qy 81 SerPheIleValPheSerThrArgGlyThrThrleuMetLysLeuThrGluAapArgGlu 100  
Db 453 TCCCTTAATGTGTCTCCACCCGAGGAACCTTAATGAACCTGAACAGAAAGAGAGAA 512  
Qy 101 GlnIleArgGlnGlyLeuGluGluLeuGlnLylasLeuProGlyGlyAapThrTyMet 120  
Db 513 CAATCCGTCAAGGCTTAGAAGAACTCCAAAGTTCTGCCAGAGAGACACTTAACATG 572  
Qy 121 HisGluGlyPheGluArgAlaSerGluGlnIleTyTyTyGluAsnArgGlnTyArg 140  
Db 573 CATGAAGATTTGAAAGGCGCAGTGAAGATTAATATGAAACAGACAAAGGTTACAGG 632  
Qy 141 ThrAlaSerValIleIleAlaLeuThrAapGlyGluLeuHisGluAapLeuPhePheTy 160  
Db 633 ACAGCCAGCGTCATCATTTGCTTGACATGAGAGAACTCCATAGAAATCTCTTTTCTAT 692  
Qy 161 SerGluArgGluAlaAsnArgSerArgAapLeuGlyValIleValTyTyCysValGlyVal 180  
Db 693 TCAAGAGGAGGCTTAATAGGTCTCGAGATCTTGTCATTTGTTACTGTGTGGTGG 752  
Qy 181 LysaapPheAengluThrglnLeuAlaarglIleAlaapSerLyAspPhIvalPhePro 200  
Db 753 AAAGATTTTCATGAGACACAGCTGGCCGGATGTGGACAGTAAGGATCATGTGTTCCC 812  
Qy 201 ValaenapGlyPheGlnAlaLeuGlnGlyIleIleHiserIleuLylasSerCys 220  
Db 813 GTGATATGACGGCTTTCAGGCTCTCGACAGCATCATCAATTTTGAGAGAGCTTGC 872  
Qy 221 IleguileuAlaAlaGluProSerThrIleCysAlaGlyIleuSerPheGlnValVal 240  
Db 873 ATCGAATATCTAGCAGCTGAACCATCCACCATATGTGAGAGAGTCAATTCAGATTGC 932  
Qy 241 ValargGlyAenglyPheargHisAlaargAsnValaapArgValIleuCySerPheLys 260  
Db 933 GTGAGAGGAAGAGGCTTCGACATGCCGCAACGTGACAGGCTCTTCGACGCTTCAG 992  
Qy 261 IleAenapSerValThrleuAenglyLylasProPheSerValGluAepThrTytleuLeu 280  
Db 993 ATCAATGACTCGGTACACTCAATAGAGAGCCCTTTCTGTGAAAGATTAATTTACTG 1052  
Qy 281 CysProAlaProIleleuLylasGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300  
Db 1053 TGTCCAGCGCTTATCTTAAAGAGTTGACATGAAGCTGCACCTCCAGGTACAGTGAAC 1112  
Qy 301 AapGlyLeuSerPheIleSerSerSerValIleIleThrThrThHisCySerLeuHis 320  
Db 1113 GATGCCCTCTCTTTATCTCCAGTTCTGTGATCATCATCACACACACACTGTAGCTTCAC 1172  
Qy 321 LysIleAlaSerGlyProThrThrAlaAlaCyMetGlu 333  
Db 1173 AAAATTGCATCAGGCCCAACACAGCTGTGCATGAGAA 1211

RESULT 5  
US-10-201-292-1  
; Sequence 1, Application US/10201292  
; Publication No. US20030144193A1  
; GENERAL INFORMATION:  
; APPLICANT: James B. ROTTMAN  
; APPLICANT: Theresa L. O'KEEFE  
; APPLICANT: Engin OZKANNAK  
; APPLICANT: Judith J. HEALEY  
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
; FILE REFERENCE: 7853-253-999

```

US-09-970-076-8 (1-333) x US-10-201-292-1 (1-2272)
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ. ID NOS: 35
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2272
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (213)...(1211)
US-10-201-292-1

Alignment Scores:
Pred. No.: 1,13e-219      Length: 2272
Score: 1728.00           Matches: 333
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 100.00%             Indels: 0
DB: 15                          Gaps: 0

```

Qy	1	MeAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnThrPheSerLeuAlaThr	20
Db	213	ATGGCCACGGCGGAGGGAGAGGCCCTCGGCATCGGCTTCAGTGGCTCTTTGGCACT	2727
Qy	21	LeuValIleuIleCysAlaIleGlyGlnGlyIaArgArgIuAerGlyIleProAlaCysTyr	40
Db	273	CTGGTGTCTCATCTGCCCGGGCAAGGGGGAGCCAGGAGAGATGGGGGGTCCAGCTGGCTAC	3323
Qy	41	GlyGlyPheAspSerLeuTyrPheIleLeuAspArgLysSerValIleuIleHisThrAsn	60
Db	333	GGCGGATTTGACCTGTGACTTTCATTATTGGCAAAATCAGAAAGTGCTGCGACCACTGGAAAT	3929
Qy	61	GluIleTyrTyrPheValGluGlnIleuAlaHisLysPheIleSerProGlnLeuArgMet	80
Db	393	GAATCATATTACTTTGGACAGATTGGGTCCAAATTCATCAGCCCACTTAGAATG	4523
Qy	81	SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAerArgGlu	100
Db	453	TCTCTTATTTGTTTCTCCACCCGAGGAAACAACTTAAAGAACTGACAGAAACAGAGAA	5121
Qy	101	GluIleArgGlnGlyLeuGluGluIleuGlnLysValLysLeuProGlnGlyAerThrTyrMet	120
Db	513	CAATTCGCTAAGCGCTAAGAGAACTCCAGAAAGTTCTGCCAGAGAGAGACATTACATG	5727
Qy	121	HisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArg	140
Db	573	CATGAGAGATTGAAAGGGCGAGTGAAGCATTTATTATGAAACAGACAAAGGTACAGG	6323
Qy	141	ThrAlaSerValIleIleAlaLeuThrArgGlyGluLeuHisGluAerPhePheTyr	160
Db	633	ACAGCCAGCGCTCATCTTGGCTTGTGATGAGAGAACTCCAGAGAGATCTCTTTTCTAT	6929
Qy	161	SerGluArgGluAlaAsnArgSerArgAerLysGlyAlaIleValTyrCysValGlyVal	180
Db	693	TCAGAGAGGAGGCTTAATAGCTTCGAGATCTTGGTCAATGTTTACTGTGTGGGTGG	7523
Qy	181	LysAspPheAsnGluThrGlnIleuAlaArgIleAlaAspSerLysAspHisValPhePro	200
Db	753	AAAGATTTCATAGACACACAGCTGGCCCGGATTTGGGACAGTAAGATCATGTGTTCCC	8121
Qy	201	ValAsnAspArgLysPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys	220
Db	813	GTGATATACGCTTTTACGGCTCTGCAAGGACATCATCTCAATTATTGAAAGATCTCTGC	8727
Qy	221	IleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyLysSerPheGlnValVal	240
Db	873	ATCGAATTTTACACAGTGAACATCCATCCAAATGTGGCAGAGAGTCAATTTCAGTGTGC	9323
Qy	241	ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys	260

Dp	993	GTGAGAGGAAACGGCTTCCGACATGCGCCGCAACGGGACGAGGATCTCTCGAGCTTCAAG	992
Qy	261	ILLeSnApSeRvAlThrLeuAsnGluYpProPheSeRvAlGluAspThrTyrLeuLeu	280
Dp	993	ATCATAGACTGGTCACACTCAATAGAGAAAGCCCTTTTCTGTGGAGAGATACTTATTTACTG	1055
Qy	281	CysProAlaPcoIleLeuLeuGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn	300
Dp	1053	TGTCCAGGCGCTTACTTTAAAGAAAGTTGGCATGAAAGCTGCATCTCAGCTCAGCATGAAAC	1112
Qy	301	AspGlyLeuSerPheIleSerSerSerValIleIleThrTrpHisCysSerLeuHis	320
Dp	1113	GATGGCCCTCTCTTTATCTCAGTTCTGTCATCATCACACACACACACTGTAGCCTCCAC	1172
Qy	321	LyS1Leu1AsnSerGlyProThrTrpAlaAlaCysMetGlu	333
Dp	1173	AAAAATTGCATCAGGCCCCACAAACAGCTGCTGCATGGAA	1211
RESULT 6			
US-10-198-846-9957			
; Sequence 9957, Application US/10198846			
; Publication No. US2003009974A1			

```

/ APPLICANT: Lillie, James
/ APPLICANT: Xu, Yongyao
/ APPLICANT: Wang, Youzhen
/ APPLICANT: Steinmann, Kathleen
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
/ TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
/ TITLE OF INVENTION: THERAPY OF BREAST CANCER
/ FILE REFERENCE: MRI-049
/ CURRENT APPLICATION NUMBER: US/10/198,846
/ CURRENT FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/306,220
/ PRIOR FILING DATE: 2001-07-18
/ NUMBER OF SEQ ID NOS: 14084
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9957
/ LENGTH: 2353
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 1, 2, 243, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351,
/ LOCATION: 2352, 2353
/ OTHER INFORMATION: n = A,T,C or G
US-10-198-846-9957

Alignment Scores:
Pred. No.: 1,2e-219 Length: 2353
Score: 1728.00 Matches: 333
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-970-076-8 (1-333) x US-10-198-846-9957 (1-2353)

QY 1 MetalathralagluarxarxalaleuuglylleglyphegintprleuSerleuAlathr 20
DB 294 ATGGCCACGGCGGCGGAGGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTGGCCACT 353
QY 21 leuValleuileCySaalaglyGlnglyGlyvarxaroggiuaparGlylProAlaCyTr 40
DB 354 CTGGTCTCATCTGTGGCGCGGCGAAGGGGAGACGACGAGGAGATGGGGGATCCAGCTGCTAC 413
QY 41 GlylylPheapleuTyrrPheileleuaplysserGlySerVallleuHleHistrPan 60
DB 414 GCGCGATTGACCTGTACTTATTTTGGACAAATCAGGAAGTGTGTCTCACCACTGGAAAT 473
QY 61 GluileTyrrTyrrPheValGluGlnleuAlaHisIuSpPheIleSerProGlnleuArgMet 80
DB 474 GAAATCTATATCTTGTGGAAACAGTGGCTCACAAATTCATCAGCCCAAGTGTGAATG 533

```

QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100  
Db 534 TCCCTTATGTTGTTTCCACCCGAGGAAACAACCTTAATGAACTGACAGAAAGACAGAA 593  
QY 101 GlnIleArgGlnGlyLeuGlnGlyLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120  
Db 594 CAATCCCTCAAGGCTTGAAGAACTCCAGAAAGTTCCAGAGGGAGACACTTACATG 653  
QY 121 HisGlnGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140  
Db 654 CATGAAGATTTGAAAGGCCAGTACAGATTTTATGAAACAGCAAGGGTACAGG 713  
QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyLeuMetGluAspLeuPhePheTyr 160  
Db 714 AAGCCACGTCATCATGCTTGTGACTGATGAGAACTCCATGAAGATCTCTTTTTCAT 773  
QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180  
Db 774 TCAGAGAGGAGGCTAATAGGCTTCAGATCTTGTGCATTTGTTTACTGTGTGTGTG 833  
QY 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200  
Db 834 AAAGATTCAATGACACACAGCTGACCCGAGTTGCGACAGTAAAGATCATGTGTTCC 893  
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220  
Db 894 GTGAATGACGGCTTCAAGCTCTCGACAGCATCATCACTCAATTTTGAAGAGTCTGCG 953  
QY 221 IleGluIleLeuAlaIleGluProSerThrIleCysValGlyGluSerPheGlnValVal 240  
Db 954 ATCGAAATTTCAAGCAGCTGAACCATCCACATATGTGAGAGAGTCAATTTCAAGTTGTC 1013  
QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260  
Db 1014 GTGAGAGAAACGGCTTCGACATCCCGCAACGTGGACAGGCTCTTGCAGCTTCAG 1073  
QY 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrLeuLeu 280  
Db 1074 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGAAAGATCTTATTACTG 1133  
QY 281 CysProAlaProIleLeuLysGlyValGlyMetLysValAlaLeuGlnValSerMetAsn 300  
Db 1134 TGTCACAGGCGCTATCTTAAAGAACTGGCATGAAGCTGCATCCAGTCAAGCATGAA 1193  
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerLeuHis 320  
Db 1194 GATGCTCTCTTTTATCTCCAGTTCTGTCTCATCATCACACACACACTGTAAGCTCCAC 1253  
QY 321 LysIleAlaSerGlyProThrThrAlaAlaCysMetGlu 333  
Db 1254 AAAATTGCATCAGGCCCAACAACAGCTGTCATGAGAA 1292

RESULT 7  
US-09-833-381-998  
Sequence 998, Application US/09833381  
Patent No. US20020132090A1  
GENERAL INFORMATION:  
APPLICANT: Robison, Keith E.  
FILE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs  
FILE REFERENCE: 5800-119  
CURRENT APPLICATION NUMBER: US/09/833,381  
CURRENT FILING DATE: 2001-04-11  
PRIOR APPLICATION NUMBER: 09/516,448  
PRIOR FILING DATE: 2000-02-29  
NUMBER OF SEQ ID NOS: 2050  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 998  
LENGTH: 2459  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature

LOCATION: (1)...(2459)  
OTHER INFORMATION: n = A,T,C or G  
US-09-833-381-998

Alignment Scores:  
Pred. No.: 1,296-219 Length: 2459  
Score: 1728.00 Matches: 333  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-970-076-8 (1-333) x US-09-833-381-998 (1-2459)

QY 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnThrPheLeuSerLeuAlaThr 20  
Db 412 ATGGCCACGGCGAGCGGAGAGCCCTCGCATCGCTTCCAGTGGCTCTCTTGGCACT 471  
QY 21 LeuValLeuIleCysAlaGlyGlnGlyIleArgArgGluAspGlyIleProAlaCysTyr 40  
Db 472 CTGGTGCTCATCTGCGCCGGCAAGGGGAGCGCAGGAGGATGGGGGTCCAGCTGCTAC 531  
QY 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTyrAsn 60  
Db 532 GCGGATTTGACCTGATCTTCAATTTTGGACAAATCAGAAAGTGTGTGCACCACTGAAT 591  
QY 61 GluIleTyrTyrPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMet 80  
Db 592 GAAATCTTATCTTGTGGAACAGTTGGCTCACAAATTCATACGCCACAGTTGAAATG 651  
QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100  
Db 652 TCCCTTATGTTTCTCCACCCGAGAAACAACCTTAATGAACTGACAGAAAGACAGAA 711  
QY 101 GlnIleArgGlnGlyLeuGlnLysLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120  
Db 712 CAATCCGTCAAGGCTTGAAGAACTCAGAAAGTTGTGACAGAGGACACTTACATG 771  
QY 121 HisGlnGlyPheGluArgAlaSerGluGlnIleTyrTyrGlnAsnArgGlnGlyTyrArg 140  
Db 772 CATGAAGATTTGAAGGGCCAGTGAAGCATTTATTTATGAACACACAGGTCACAG 831  
QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPheTyr 160  
Db 832 ACAGCCAGCTCATCATGCTTTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTAT 891  
QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180  
Db 892 TCAGAGAGGAGGCTAATAGGCTTCGAGATCTGTGTCAATTTGTTACTGTGTGTGTG 951  
QY 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200  
Db 952 AAAGATTTCATGAGACACAGCTGGCCGAGATTCGGAACGTAAAGATCATGTGTTCCC 1011  
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220  
Db 1012 GTGAATGACGGCTTCAAGCTCTGCAAGGATCATCACTCAATTTTGAAGAAAGTCTGCG 1071  
QY 221 IleGluIleLeuAlaIleGluProSerThrIleCysValGlyGluSerPheGlnValVal 240  
Db 1072 ATCGAAATTTCAAGAGCTGAACCATCCACATATGTGACAGAGAGTCAATTTCAAGTTGTC 1131  
QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260  
Db 1132 GTGAGAGAAACGGCTTCCAGATGCCCGAAGTGAACAGGCTCTCTGACGTTCAAG 1191  
QY 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrLeuLeu 280  
Db 1192 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGAAAGATCTTATTACTG 1251  
QY 281 CysProAlaProIleLeuLysGlyValGlyMetLysValAlaLeuGlnValSerMetAsn 300  
Db 1252 TGTCACAGGCTTATCTTAAAGAAAGTTGGCATGAAGCTGCACTCCAGTCCAGCATGAAC 1311



QY 301 AepgIleuSerPheIleSerSerValIleIleThrThrHiCySerIeuHis 320  
DB 1312 GATGCCCTCTCTTTATCTCCAGTTCTGTCAATCAACACACACACTGTAGCTCCAC 1371  
QY 331 LysIleAaSerGlyProThrThrAlaAcyMetGlu 333  
DB 1372 AAAATTGCATCAGGCCCAACACAGCTGCTTCATGAA 1410

RESULT 8  
US-10-038-307-23  
/ Sequence 23, Application US/10038307  
/ Publication No. US20030134786A1  
/ GENERAL INFORMATION:  
/ APPLICANT: James B. ROTTMAN  
/ APPLICANT: Theresa L. O'KEEFE  
/ APPLICANT: Englin OZKAYNAK  
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
/ FILE REFERENCE: 7853-253-999  
/ CURRENT APPLICATION NUMBER: US/10/038,307  
/ NUMBER OF SEQ ID NOS: 26  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 23  
/ LENGTH: 1056  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
US-10-038-307-23

Alignment Scores:  
Pred. No.: 6,89e-219 Length: 1056  
Score: 1718.00 Matches: 332  
Percent Similarity: 99.70% Conservative: 0  
Best Local Similarity: 99.70% Mismatches: 1  
Query Match: 99.42% Indels: 0  
DB: 15 Gaps: 0

US-09-970-076-8 (1-333) x US-10-038-307-23 (1-1056)

QY 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerIeuAlaThr 20  
DB 13 ATGGCAGCGGCGAGCGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTTTGGCCACT 72  
QY 21 LeuValIleuIleCyAlaGlyGlnGlyAlaArgArgIleGlyProAlaCySerTy 40  
DB 73 CTGGGCTCATCTGGCGCGGCGAGCGGCGAGCGAGTGGGCTCCAGCTGCTAC 132  
QY 41 GlyGlyPheAapLeuTyPheIleuAapLySerGlySerValIleuHisIleTrpAsn 60  
DB 133 GCGGATTTGACCTTACTTCTTCTTTGACAAATCAAGAAAGTGTGCTGCACACCTGAAAT 192  
QY 61 GluIleTyTyPheValGlnIleuAlaHisIlePheIleSerProGlnIleuArgMet 80  
DB 193 GAATCTATTACTTGTGGAAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAAGATG 252  
QY 81 SerPheIleValPheSerThrArgIleThrIleuMetIleValIleuThrGluAapArgIle 100  
DB 253 TCCCTTATTGTTTCTCCACCCGAGAAACAACTTAAGAACTGACAGAAACAGAGAA 312  
QY 101 GlnIleArgGlnGlyLeuGlnIleuGlnIleuValIleuProGlyGlyAapThrTyMet 120  
DB 313 CAATTCGCTCAAGGCTTGAAAGAACTCCAGAAAGTTCGCAAGAGAGACCTTACATG 372  
QY 121 HisGlnGlyPheGluArgAlaSerGlnIleTyTyTyGluAsnArgGlnGlyTyArg 140  
DB 373 CATGAAGATTGAAAGGCGCAGTGAGAGATTATTATGAAACAGCAAGGATCAGG 432  
QY 141 ThrAlaSerValIleIleAlaIleuThrArgArgIleGluLeuHisGlnAapLeuPheTy 160  
DB 433 ACAGCAGAGCTCATATGCTTGTGCTGATGAGAACTCCATGAAGATCTCTTTTTCAT 492  
QY 161 SerGluArgGluAlaAsnArgSerArgAapLeuGlyAlaIleValTyCySerValGlyVal 180

DB 493 TCAGAGAGAGAGGCTAATAGCTCTGAGATCTGGTGCATTTGTTACTGTGTGTG 552  
QY 181 LysAapPheAaGlnThrGlnIleuAlaArgIleAlaAapSerLyAapHisValPhePro 200  
DB 553 AAAGATTTCATATGAGACACACTGGCCGAGATGGGACAGTAAGATCATGTGTTCC 612  
QY 201 ValAaAapGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIleLySerCys 220  
DB 613 GTGAATGACGGCTTCAAGGCTCTGCAGGCAATCATCTCAATTTTAAAGAGCTTGC 672  
QY 221 IleGluIleuAlaIleGluProSerThrIleCyAlaGlyGlySerPheGlnValVal 240  
DB 673 ATCGAATTTCTAGAGCTGGAACCATCCACCAATATGACAGAGAGATCTTCAAGTTC 732  
QY 241 ValArgGlyAaGlnGlyPheArgHisAlaArgAsnValAapArgValIleuCySerPheLy 260  
DB 733 GTGAGAGGAAACGGCTTCGACATGCCGCAACGTGACAGAGTCTCTGCAGCTTCAAG 792  
QY 261 IleAaAapSerValThrIleuAaGlnIleuPheProPheSerValIleuAapThrTyIleu 280  
DB 793 ATCAATGACTGGTCACTCAATGAGAAAGCCCTTTCTGGAGAGATATTATTACTG 852  
QY 281 CysProAlaProIleuLeuGlyValGlyMetLyAlaAlaLeuGlnValSerMetAsn 300  
DB 853 TGTCCAGCGCTATCTTAAAGAGTTGCGATGAAGTGCACCTCAGTCAAGTCAAGAAC 912  
QY 301 AepGlyLeuSerPheIleSerSerValIleIleThrThrHiCySerIeuHis 320  
DB 913 GATGCCCTCTCTTTATCTCCAGTTCTGTCAATCAACACACACACTGTAGCTCCAC 972

RESULT 9  
US-10-201-292-23  
/ Sequence 23, Application US/10201292  
/ Publication No. US20030144193A1  
/ GENERAL INFORMATION:  
/ APPLICANT: James B. ROTTMAN  
/ APPLICANT: Theresa L. O'KEEFE  
/ APPLICANT: Englin OZKAYNAK  
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
/ FILE REFERENCE: 7853-253-999  
/ CURRENT APPLICATION NUMBER: US/10/201,292  
/ NUMBER OF SEQ ID NOS: 36  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 23  
/ LENGTH: 1056  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
US-10-201-292-23

Alignment Scores:  
Pred. No.: 6,89e-219 Length: 1056  
Score: 1718.00 Matches: 332  
Percent Similarity: 99.70% Conservative: 0  
Best Local Similarity: 99.70% Mismatches: 1  
Query Match: 99.42% Indels: 0  
DB: 15 Gaps: 0

US-09-970-076-8 (1-333) x US-10-201-292-23 (1-1056)

QY 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerIeuAlaThr 20  
DB 13 ATGGCAGCGGCGAGCGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTTTGGCCACT 72  
QY 21 LeuValIleuIleCyAlaGlyGlnGlyAlaArgArgIleGlyProAlaCySerTy 40  
DB 73 CTGGGCTCATCTGGCGCGGCGAGCGGCGAGTGGGCTCCAGCTGCTAC 132

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Oy 41 GlyGlyPheAspLeuTyrPheIleuAspLysSerGlySerValIleuHisIleTPasn 60
Db 133 GGGCGATTGACCTGACTTCTCATTTTGGACAAATCAGAAAGTGTCTGCACACTGGAA 192
Oy 61 GluIleTyrTyrPheValGluGlnLeuAlaHisIleValPheIleSerProGlnLeuArgMet 80
Db 193 GAAATCTATTACTTTGTGGAAACAGTTGGCTCAAAATTCATCAGCCCACTGTGGAAATG 252
Oy 81 SerPheIleValPheSerThrArgGlyThrThrIleuMetLysLeuThrGluAspArgGlu 100
Db 253 TCCTTATTTGTTTCTCCACCCGAGAACACCTTAATGAATCTGACAGAAAGACAGAA 312
Oy 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120
Db 313 CAATCCGTCAGAGGCTAGAAAGAACTCCAGAAAGTTCTCCAGAGAGAGACACTTACAC 372
Oy 121 HisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAspArgGlnGlyTyrArg 140
Db 373 CATGAAAGATTGAAAGGGCCAGTCAGACAGATTATTAATGAAAACAGACAGGGTACAG 432
Oy 141 ThrIleSerValIleIleAlaLeuThrAspGlyGluMetHisGluAspLeuPhePheTyr 160
Db 433 ACAGCACCGTCATCTATTGCTTTGACTATGAGAACTCCAGAAATCTCTTTTCTAT 492
Oy 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
Db 493 TCAGAGAGGAGGCGTAATAGCTTCGAGATCTTGCTGCAATTTGTTTACTGTGTGGTGTG 552
Oy 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
Db 553 AAAGATTCATATGAGACACAGCTGCCCGGATGGCGACAGTAAGATCATGTGTTTCCC 612
Oy 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220
Db 613 GTGAATGACGGCTTTCAGGCTCTGCAAGGCAATCATCCACTCAATTTTGAAGAAGCTCTGC 672
Oy 221 IleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGlySerPheGlnValVal 240
Db 673 ATCGAAATTTCTAGACGCTGAAACCATCCACATATGTGAGAGAGTCACTTTCAAGTTGTC 732
Oy 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
Db 733 GTGAGAGGAAACGGCTTCCGACATGCCCGCAACGGGACAGGGTCTCTGCAAGCTTCAAG 792
Oy 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrLeuLeu 280
Db 793 ATCATGACTCGGTCACTCATATGAGAAAGCCCTTTCTGTGGAAGATTAATTATTTACTG 852
Oy 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
Db 853 TGTCCAGCGCTATCTTAAAGAGAGTTGGCATGAAAGTGCATCCAGTCCAGTCAAGTGAAC 912
Oy 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerLeuHis 320
Db 913 GATGCCCTCTCTTTATCTCCAGTTCTGTCTCATCATCACACACACACTGTAGCTCCAC 972
Oy 321 LysIleAlaSerGlyProThrThrAlaIaCysMetGlu 333
Db 973 AAAATTGCATCGGCCCCACACACAGCTCTTCATGAGAA 1011

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RESULT 10  
US-10-038-307-21

```

; Sequence 21, Application US/10038307
; Publication NO. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTHMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038.307

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; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PASTESEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-21

Alignment Scores:
Pred. No.: 2,71e-218 Length: 1047
Score: 1713.50 Matches: 333
Percent Similarity: 97.37% Conservative: 0
Best Local Similarity: 97.37% Mismatches: 9
Query Match: 99.16% Indels: 9
DB: 15 Gaps: 1

US-09-970-076-8 (1-333) x US-10-038-307-21 (1-1047)
Oy 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
Db 13 ATGGCCACGGCGGAGCGGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTGGCCACT 72
Oy 21 LeuValLeuIleCysAlaGlyGlnGlyIleArgArgGluAspGlyGlyPro----- 37
Db 73 CTGGTCTCATCTGCGCGCGGCAAGGGGACGACGAGAGATGGGGGTCCAATGCAATTAC 132
Oy 38 -----AlaCysTyrGlyGlyPheAspLeuTyrPheIleLeuAspLys 51
Db 133 AAGATACCATGACCAAGGCGCTGACGGGATTTACCTGTACTTCACTTTTGGACAAA 192
Oy 52 SerGlySerValLeuHisIleTPasnGluIleTyrTyrPheValGluGlnLeuAlaHis 71
Db 193 TCAGGAAGTGTGCGACCACTGGAATGAATCTATTCTTGGAAACAGTTGGCTCAC 252
Oy 72 LysPheIleSerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThr 91
Db 253 AAATTCATCAGCCCAACAGTTGAGATGTCTTTATTTTCTCCACCCGAGAAACACC 312
Oy 92 LeuMetLysLeuThrGluAspArgGluGlnIleAspGlnGlyLeuGlnLys 111
Db 313 TTAATGAATCTGACAGAAAGACAGAAACAAATCCGTCAAGGCTCAGAAACCTCAGAAA 372
Oy 112 ValLeuProGlyGlyAspThrTyrMetHisGluGlyPheGluArgAlaSerGluGlnIle 131
Db 373 GTTCTGCAAGAGAGACACTTACATGATGAAGATTGAAAGGCGCAAGTGAACAGATT 432
Oy 132 TyrTyrGluAsnArgGlnGlyTyrArgThrAlaSerValIleIleAlaLeuThrAspGly 151
Db 433 TATTATGAAAACAGACAAAGGTTACAGACAGCCGCTCATCTTGTGACTGATGGA 492
Oy 152 GluLeuHisGluAspLeuPhePheTyrSerGluArgGluAlaAsnArgSerArgAspLeu 171
Db 493 GAATTCATGAAGATCTCTTTCTATTCAAGAGGAGGCTTAATAGTCTTCGAGATCTT 552
Oy 172 GlyAlaIleValTyrCysValGlyValIleAspPheAsnGluThrGlnLeuAlaArgIle 191
Db 553 GGTGCATTTGTTTACTGTGTGGTGAAGATTTCATATGACACAGCTGGCCGGATT 612
Oy 192 AlaAspSerLysAspHisValPheProValAsnAspGlyPheGlnAlaLeuGlnGlyIle 211
Db 613 GCGGACAGTAAGATCATGTGTTTCCCGTGAATGACGGCTTTCAGGCTCAGCAAGGATC 672
Oy 212 IleHisSerIleLeuLysLysSerCysIleGlnIleLeuAlaAlaGluProSerThrIle 231
Db 673 ATCCACTCAATTTTGAAGAGTCTCTGCATGAAATTTAGAGGTGAACCATCCACATA 732
Oy 232 CysAlaGlyGlySerPheGlnValIleValArgGlyAsnGlyPheArgHisAlaArgAsn 251
Db 733 TGTCCAGAGAGATCATTTCAAGTTGTGTGAGAGAAACGGCTTCCAGATCCCGGCAAC 792
Oy 252 ValAspArgValLeuCysSerPheLysIleAsnAspSerValThrLeuAsnGluLysPro 271

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Best Local Similarity: 97.26% Mismatches: 2  
 Query Match: 95.52% Indels: 5  
 DB: 15 Gaps: 1

US-09-970-076-8 (1-333) x US-10-038-307-17 (1-1674)

QY 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20  
 DB 13 ATGGCCAGGCGGAGGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTTTGGCCACT 72  
 QY 21 LeuValLeuIleCysAlaGlyGlnGlyArgAlaGlyLeuArgGlyProAlaCysThr 40  
 DB 73 CTGGCTCATCTGGCCGGGCAAGGAGGACGCGAGAGATGGGGGTCCAGCTGTAC 132  
 QY 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60  
 DB 133 GGGCGATTGACCTTACTTCTTTTGGACAAATCAGAAAGTGTCTCACCACCTGGAAAT 192  
 QY 61 GluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80  
 DB 193 GAAATCTATTACTTGTGGACAGTTGGCTCACAATTCATCAGCCACAGTTGGAATG 252  
 QY 81 SerPheIleValPheSerThrArgIleThrThrLeuMetLysLeuThrGluAspArgGlu 100  
 DB 253 TCCTTATTGTTTCTCCACCCGAGAAACACCTTAATGAACCTGACGAAGACAGAGAA 312  
 QY 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120  
 DB 313 CAATCCGTCAAGGCTGAGAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATG 372  
 QY 121 HisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140  
 DB 373 CATGAAGATTTGAAAGGCGCCAGTAGCAGATTTTGTGAAACAGACAAAGGATACAG 432  
 QY 141 ThrIleSerValIleIleAlaLeuThrAspGlyGlyLeuHisIleGluAspLeuPhePheTyr 160  
 DB 433 ACAGCCAGCGTCATATGCTTGTGACTATGAGAACTCCAGTGAAGATCTCTTTTCTAT 492  
 QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180  
 DB 493 TCAGAGAGGAGGCTAATAGCTCTGAGATCTGGTGCATTTGTTACTGTGTGGTGTG 552  
 QY 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200  
 DB 553 AAAGATTTCAATGAGACACAGCTGGCCGGATTCGGCAGATGAAGATCATGTGTTCC 612  
 QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220  
 DB 613 GTGAATGACGGCTTTCAGGCTCTTCAGAGGATCATCTCAATTTTGAAGAAGCTTCGC 672  
 QY 221 IleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyLysSerPheGlnValVal 240  
 DB 673 ATCGAAATTTCTAGCGCTGAAACATCCACATATGTGAGAGAGTCTATTCAAGTTGTC 732  
 QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260  
 DB 733 GTGAGAGGAAACGCGCTTCGACATCCCGCAACGTGGACAGGGTCTCTGCAGCTTCAAG 792  
 QY 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrLeuLeu 280  
 DB 793 ATCAATGACTGGTACACTCATATAGAAAGCCCTTTCTGTGAAAGATTAATTATTACTG 852  
 QY 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300  
 DB 853 TGTCCAGGCGCTATCTTAAAGAACTTGGCATGGAAGCTGCATCCAGGTACAGTAGAAC 912  
 QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerLeuHis 320  
 DB 913 GATGCGCTCTCTTATCTCCAGTTCTGTGCATCATCACACACACACTGTTCT----- 966  
 QY 321 LysIleAlaSerGlyProThrThrAla 329  
 DB 967 -----GACGGTCCAAATCTTCT 984

RESULT 13  
 US-10-201-292-17  
 ; Sequence 17, Application US/10201292  
 ; Publication No. US2003014193A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: James B. ROTTMAN  
 ; APPLICANT: Theresa L. O'KEEFE  
 ; APPLICANT: Engin OZKAYNAK  
 ; APPLICANT: Judith J. HEALEY  
 ; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
 ; FILE REFERENCE: 7853-253-999  
 ; CURRENT FILING DATE: 2003-02-14  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 17  
 ; LENGTH: 1674  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-201-292-17

Alignment Scores:  
 Pred. No.: 1,566-209 Length: 1674  
 Score: 1650.50 Matches: 320  
 Percent Similarity: 97.87% Conservative: 2  
 Best Local Similarity: 97.26% Mismatch: 2  
 Query Match: 95.52% Indels: 5  
 DB: 15 Gaps: 1

US-09-970-076-8 (1-333) x US-10-201-292-17 (1-1674)

QY 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20  
 DB 13 ATGGCCAGGCGGAGGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTTTGGCCACT 72  
 QY 21 LeuValLeuIleCysAlaGlyGlnGlyArgAlaGlyLeuArgGlyProAlaCysThr 40  
 DB 73 CTGGCTCATCTGGCCGGGCAAGGAGGACGCGAGAGATGGGGGTCCAGCTGTAC 132  
 QY 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60  
 DB 133 GGGCGATTGACCTTACTTCTTCACCCGAGAAACACCTTAATGAACCTGACGAAGACAGAGAA 312  
 QY 61 GluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80  
 DB 193 GAAATCTATTACTTGTGAGAACTCCAGTGAAGATTTGTTGACAAATTCATCAGCCACAGTTAGAAATG 252  
 QY 81 SerPheIleValPheSerThrArgIleThrThrLeuMetLysLeuThrGluAspArgGlu 100  
 DB 253 TCCTTATTGTTTCTCCACCCGAGAAACACCTTAATGAACCTGACGAAGACAGAGAA 312  
 QY 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120  
 DB 313 CAATCCGTCAAGGCTGAGAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATG 372  
 QY 121 HisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140  
 DB 373 CATGAAGATTTGAAAGGCGCCAGTAGCAGATTTTGTGAAACAGACAAAGGATACAG 432  
 QY 141 ThrIleSerValIleIleAlaLeuThrAspGlyGlyLeuHisIleGluAspLeuPhePheTyr 160  
 DB 433 ACAGCCAGCGTCATATGCTTGTGACTATGAGAACTCCAGTGAAGATCTCTTTTCTAT 492  
 QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180  
 DB 493 TCAGAGAGGAGGCTAATAGCTCTCGAGATCTGGTGCATTTGTTACTGTGTGGTGTG 552  
 QY 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200  
 DB 553 AAAGATTTCAATGAGACACAGCTGGCCGGATTCGGCAGATGAAGATCATGTGTTTCCC 612  
 QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220

Db 613 GTGATGACGGCTTCAAGCTCTGCAGAGCATCATCCACTCAATTTTGAGAAAGTCCCTGC 672  
Qy 221 IIEGIIIELEUAIAAGIUPROSETHIIEYSAIAGIYGLUSERPHEGINVAIAI 240  
Db 673 ATCGAAATTTCTGACAGCTGMAACCATTCATATGCGAGAGATCTCAATTTCAATTTGTC 732  
Qy 241 VALAARGIYAANGIYPHEARHIAIARGAENVIAAPARGVALIEUCYSESERPHELYS 260  
Db 733 GTGAGAGGAAACGGCTTCGACATGCCCAACGTGACAGGGCTCTCTGCAGCTTCAAG 792  
Qy 261 IIEAENAPSERVALTHREUANGIULYSPROPHESERVALIGUASPHTHYRTHREUEN 280  
Db 793 ATCAATGACTCGCTCACTCACTCAATGAGAACCCCTTTCTGTGAGAAATCTTATTTACTG 852  
Qy 281 CYPROAIAPROIIIELEULYAGIUMETLYSAIAIALEUGINVAISERNECAN 300  
Db 853 TGTCCAGCGCTATCTTAAAGAGATTGGCATGAAGCTGCACCTCAGGTCCAGATGAAAC 912  
Qy 301 AARGIYLEUSERPHEIIIESESERSERVALIIIEIETHRTHRHICYSERIEUHI 320  
Db 913 GATGACCTCTCTTTATCTCCAGTTCTGTGCATCATCAACCAACACACTGTTCT----- 966  
Qy 321 LYSAIEAIAESERGIYPROTHRTHTA 329  
Db 967 -----GACGCTCCAAATCTTCT 984  
RESULT 14  
US-10-133-937-58  
; Sequence 58, Application US/10133937  
; Publication No. US20030207278A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltzer, Paul  
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,  
; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND  
; FILE REFERENCE: OTHER BIOLOGICAL STATES  
; CURRENT APPLICATION NUMBER: US/10/133,937  
; CURRENT FILING DATE: 2002-11-04  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 58  
; LENGTH: 1454  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-133-937-58  
Alignment Scores:  
Pred. No.: 1,966-209 Length: 1454  
Score: 1649.00 Matches: 318  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 95.43% Indels: 0  
DB: 16 Gaps: 0  
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Qy 21 LEUVALLEUIECYALAGIYINGIYGIATGATGGLUAPSGIYGIYPROAIACYSYR 40  
Db 204 CTGGGTCTATCTGGCGCGGAGGAGGAGCCAGGAGAGATGGGGGTCTCACTGCTAC 263  
Qy 41 GIYGIYPHEAPLEUTYRPHIELEUAAPLYSERGIYSERVALIEUHIETHRPHAN 60  
Db 264 GCGGATTTGACCTGTAATCTTTTGGCAAAATCAGAAAGTGTCTGCACCACTGGAAT 323  
Qy 61 GIIIEYTYRPHIEVALIUGIINLEUAIETHLYRPHIELESEPRGIIINLEUARGHET 80

Db 324 GAANTCTATTCTTTGTGGAACAGTTGGCTCACAAAATTCATCAAGCCACAGTTGGAATG 383  
Qy 81 SERPHEIIIEALPHESETHRTARGIYTHRTHEUWETLYLEUTHRTGLUAPARGIU 100  
Db 384 TCTTTATTTGTTTCTCCACCCGAGGAACAACCTTAATGAACATGACAGAAACAGAA 443  
Qy 101 GIIIEAARGIYINGIYLEUGIINLEUENIINYSVALIEUPROGIYGIYASPTHTYRTHET 120  
Db 444 CAANTCCGTCAAGGCTTGAAGAACTCCAAAGTTCTCCAGAGGAGACATTTACTAC 503  
Qy 121 HIEGIIYIYPHEGIUARGAIAESERGIUGIINIEYTYRGIYUASNARGIYIYARG 140  
Db 504 CATGAGATTTGAAAGGCCAGTGAAGCATTTATTTGAAAACAGCAAGGGATGACAG 563  
Qy 141 THRALSERVALIIIEALIEUETHRAPHGIYGLIEUHIAGIUPLEUPHEPHTYR 160  
Db 564 ACAGCCAGCGTATCATATGCTTTGATGATGAGAACTCCATGAAGATCTCTTTTCTAT 623  
Qy 161 SERGIUARGIUAIAENARGSERARGAPLEUGIYAIIEVALTYRQYVALIYVAI 180  
Db 624 TCAGAGAGGAGGCTTAATGAGTCTCGAGATCTGTGCAATTTGTTACTGTGTGTGTG 683  
Qy 181 LYSAEPHEAANGIUTHTGINLEUAIARGIIEALIAEPSERLYSAAPHIEVALPHEPRO 200  
Db 684 AAAGATTTCAATGAGACACACACTGGCCCGATTGGGACATGAAGATCATGTGTTTCC 743  
Qy 201 VALAENAPGIYPHEGINAIALEUGIYIIIEIIEHISERIIIELEUAYLESERCY 220  
Db 744 GTGAATGACGGCTTCAAGCTCTCGAAGCATCATCTCAATTTTGAAGAAGCTCTGC 803  
Qy 221 IIEGIIIELEUAIAAGIUPROSETHRIIEYSAIAGIYGLUSERPHEGINVAIAI 240  
Db 804 ATCGAAATTTTGAAGCTGAAACCATCCCATATGTGAGAGAGTCAATTTCAAGTTTC 863  
Qy 241 VALAARGIYAANGIYPHEARHIAIARGAENVIAAPARGVALIEUCYSESERPHELYS 260  
Db 864 GTGAGAGGAAACGGCTTCGACATGCCCAACGTGACAGGGCTCTGACAGCTTCAAG 923  
Qy 261 IIEAENAPSERVALTHREUANGIULYSPROPHESERVALIGUASPHTHYRTHREUEN 280  
Db 924 ATCAATGACTCGGTCACTCAATGAGAGCCCTTTCTGTGAGAAACATTAATTTACTG 983  
Qy 281 CYPROAIAPROIIIELEULYAGIUMETLYSAIAIALEUGINVAISERNECAN 300  
Db 984 TGTCCAGCGCTATCTTAAAGAGTTGGCATGAAGCTGCACCTCCAGTCAAGATGAAAC 1043  
Qy 301 AARGIYLEUSERPHEIIIESESERSERVALIIIEIETHRTHRHICYSER 318  
Db 1044 GATGACCTCTCTTTATCTCCAGTTCTGTGCATCATCAACCAACACACTGTTCT 1097  
RESULT 15  
US-10-159-563-58  
; Sequence 58, Application US/10159563  
; Publication No. US20040009154A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltzer, Paul  
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS  
; FILE REFERENCE: 11613.56US11  
; CURRENT APPLICATION NUMBER: US/10/159,563  
; PRIOR APPLICATION NUMBER: US 10/133,937  
; PRIOR FILING DATE: 2002-12-09  
; NUMBER OF SEQ ID NOS: 444  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 58  
; LENGTH: 1454  
; TYPE: DNA  
; ORGANISM: Homo sapiens



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OM protein - protein search, using sw model

Run on: June 21, 2004, 13:39:51 / Search time 12.5745 Seconds

(without alignments)  
1367.166 Million cell updates/sec

Title: US-09-970-076-8

Perfect score: 1728  
Sequence: 1 MATERRALGICFQWLSLAT.....TTHCSIMKIASGPTTACME 333

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Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents AA:

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4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*  
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6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	166	9.6	1155	1 US-08-286-889-46	Sequence 46, Appl
2	166	9.6	1155	1 US-08-485-618-46	Sequence 46, Appl
3	166	9.6	1155	1 US-08-362-652-46	Sequence 46, Appl
4	166	9.6	1155	2 US-08-605-672-46	Sequence 46, Appl
5	166	9.6	1155	2 US-08-482-293A-46	Sequence 46, Appl
6	166	9.6	1155	2 US-08-943-363-46	Sequence 46, Appl
7	166	9.6	1155	3 US-09-193-043-46	Sequence 46, Appl
8	166	9.6	1155	4 US-09-688-307A-46	Sequence 46, Appl
9	166	9.6	1155	4 US-09-350-259-46	Sequence 46, Appl
10	166	9.6	1161	1 US-08-485-618-53	Sequence 53, Appl
11	166	9.6	1161	1 US-08-362-652-53	Sequence 53, Appl
12	166	9.6	1161	2 US-08-605-672-53	Sequence 53, Appl
13	166	9.6	1161	2 US-08-482-293A-53	Sequence 53, Appl
14	166	9.6	1161	2 US-08-943-363-53	Sequence 53, Appl
15	166	9.6	1161	3 US-09-193-043-53	Sequence 53, Appl
16	166	9.6	1161	4 US-09-688-307A-53	Sequence 53, Appl
17	166	9.6	1161	4 US-09-350-259-53	Sequence 53, Appl
18	159.5	9.2	1151	1 US-08-286-889-37	Sequence 37, Appl
19	159.5	9.2	1151	1 US-08-485-618-37	Sequence 37, Appl
20	159.5	9.2	1151	1 US-08-362-652-37	Sequence 37, Appl
21	159.5	9.2	1151	2 US-08-605-672-37	Sequence 37, Appl
22	159.5	9.2	1151	2 US-08-482-293A-37	Sequence 37, Appl
23	159.5	9.2	1151	2 US-08-943-363-37	Sequence 37, Appl
24	159.5	9.2	1151	3 US-09-193-043-37	Sequence 37, Appl
25	159.5	9.2	1151	4 US-09-688-307A-37	Sequence 37, Appl
26	159.5	9.2	1151	4 US-09-350-259-37	Sequence 37, Appl
27	159.5	9.2	1161	1 US-08-173-497-2	Sequence 2, Appl

28	159.5	9.2	1161	1 US-08-286-889-2	Sequence 2, Appl
29	159.5	9.2	1161	1 US-08-485-618-2	Sequence 2, Appl
30	159.5	9.2	1161	1 US-08-362-652-2	Sequence 2, Appl
31	159.5	9.2	1161	1 US-08-605-672-2	Sequence 2, Appl
32	159.5	9.2	1161	1 US-08-482-293A-2	Sequence 2, Appl
33	159.5	9.2	1161	1 US-08-943-363-2	Sequence 2, Appl
34	159.5	9.2	1161	2 US-08-605-672-2	Sequence 2, Appl
35	159.5	9.2	1161	2 US-08-482-293A-2	Sequence 2, Appl
36	159.5	9.2	1161	2 US-08-943-363-2	Sequence 2, Appl
37	159.5	9.2	1161	2 US-08-605-672-2	Sequence 2, Appl
38	159.5	9.2	1161	2 US-08-482-293A-2	Sequence 2, Appl
39	159.5	9.2	1161	2 US-08-943-363-2	Sequence 2, Appl
40	159.5	9.2	1161	2 US-08-605-672-2	Sequence 2, Appl
41	159.5	9.2	1161	2 US-08-482-293A-2	Sequence 2, Appl
42	159.5	9.2	1161	2 US-08-943-363-2	Sequence 2, Appl
43	159.5	9.2	1161	2 US-08-605-672-2	Sequence 2, Appl
44	159.5	9.2	1161	3 US-09-193-043-2	Sequence 2, Appl
45	159.5	9.2	1161	3 US-09-688-307A-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-08-286-889-46  
Sequence 46, Application US/08286889  
Patent No. 5470953  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Mich  
APPLICANT: Van der Vliet, Monica  
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Seair Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/286, 889  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: P38,659  
REFERENCE/DOCKET NUMBER: 27866/32168  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1155 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-286-889-46  
Query Match 9.6%, Score 166, DB 1, Length 1155;  
Best Local Similarity 28.2%, Pred. No. 3.4e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;  
37 PACYG-GDLYFIIDKSGSV-LHHMNEIYYVEQIAHKEFISPOLRMSFVSTGTTLMK 94

Db 144 PECGQEMDIAPFLDGSISIDSDFTQMKDFVKALMGQLASTSTSPSIMOYSNILKTHFT 203  
Qy 95 LTEDR-----EQIRQGLEBLQKVLPGDPTVMHGFERASBOIYYENRQGYRTA-SVITAL 148  
Db 204 FTEFKSSLSPOSLVAIVQLO-----GLTYTASGIQKVVELFHSKNGARKSAKKILIVI 258  
Qy 149 TDGELHDLFFYSE--REANRSRDLGAIIVYCVGKD-FNE-TOLARI-----ADSKDHVF 199  
Db 259 TDGQKFRDPLEYRHHVPEAEKA---GIIRYALGVGDAREPTALQELNTIGSAPSOQHV 315  
Qy 200 PVNDGFOALQGIHSHILKKSCEIILAEPSITCAGESFOVVVRNGGFRHARNVD 253  
Db 316 KVGK-FVALRSIQROIQEK---IFAIGTESRSSSSFQHEMSQGFSSALSMD 364

## RESULT 2

US-08-485-618-46  
; Sequence 46, Application US/08485618  
; Patent No. 5728533  
; GENERAL INFORMATION:  
; APPLICANT: Gallatin, W. Michael  
; APPLICANT: Van der Vlieten, Monica  
; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 South Wacker Drive, 6300 Seear Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,618  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/173,497  
; FILING DATE: 23-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/286,889  
; FILING DATE: 5-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/362,652  
; FILING DATE: 21-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams Jr., Joseph A.  
; REGISTRATION NUMBER: 38,659  
; REFERENCE/DOCKET NUMBER: 27866/32797  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; TELEFAX: 312-474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 46:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1155 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-485-618-46

Query Match 9.6%; Score 166; DB 1; Length 1155;  
Best Local Similarity 28.2%; Pred. No. 3,4e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;  
Qy 37 PACYG-GPDLYFIILKSGSV-LHHMNEIYFVEQLAHKFIISPOLRMSTFVSTGTTLMK 94  
Db 144 PECGQEMDIAPFLDGSISIDSDFTQMKDFVKALMGQLASTSTSPSIMOYSNILKTHFT 203

Qy 95 LTEDR-----EQIRQGLEBLQKVLPGDPTVMHGFERASBOIYYENRQGYRTA-SVITAL 148  
Db 204 FTEFKSSLSPOSLVAIVQLO-----GLTYTASGIQKVVELFHSKNGARKSAKKILIVI 258  
Qy 149 TDGELHDLFFYSE--REANRSRDLGAIIVYCVGKD-FNE-TOLARI-----ADSKDHVF 199  
Db 259 TDGQKFRDPLEYRHHVPEAEKA---GIIRYALGVGDAREPTALQELNTIGSAPSOQHV 315  
Qy 200 PVNDGFOALQGIHSHILKKSCEIILAEPSITCAGESFOVVVRNGGFRHARNVD 253  
Db 316 KVGK-FVALRSIQROIQEK---IFAIGTESRSSSSFQHEMSQGFSSALSMD 364

## RESULT 3

US-08-362-652-46  
; Sequence 46, Application US/08362652  
; Patent No. 576850  
; GENERAL INFORMATION:  
; APPLICANT: Gallatin, W. Michael  
; APPLICANT: Van der Vlieten, Monica  
; TITLE OF INVENTION: No. 576850el Human 2 Integrin Alpha Subunit  
; NUMBER OF SEQUENCES: 93  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 South Wacker Drive, 6300 Seear Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/362,652  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/173,497  
; FILING DATE: 23-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/286,889  
; FILING DATE: 5-AUG-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams Jr., Joseph A.  
; REGISTRATION NUMBER: 38,659  
; REFERENCE/DOCKET NUMBER: 27866/32391  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; TELEFAX: 312-474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 46:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1155 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-362-652-46

Query Match 9.6%; Score 166; DB 1; Length 1155;  
Best Local Similarity 28.2%; Pred. No. 3,4e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;  
Qy 37 PACYG-GPDLYFIILKSGSV-LHHMNEIYFVEQLAHKFIISPOLRMSTFVSTGTTLMK 94  
Db 144 PECGQEMDIAPFLDGSISIDSDFTQMKDFVKALMGQLASTSTSPSIMOYSNILKTHFT 203  
Qy 95 LTEDR-----EQIRQGLEBLQKVLPGDPTVMHGFERASBOIYYENRQGYRTA-SVITAL 148  
Db 204 FTEFKSSLSPOSLVAIVQLO-----GLTYTASGIQKVVELFHSKNGARKSAKKILIVI 258  
Qy 149 TDGELHDLFFYSE--REANRSRDLGAIIVYCVGKD-FNE-TOLARI-----ADSKDHVF 199



Db 259 TDGQFRPDLRYHVIPEAKA---GIRYALGVGDARFEPALQELNTIGSAPSQDHVF 315  
QY 200 PVNDGFOALQGIHSHILKKSCEIILAAEPSTTCAGESQVAVVNGGFRHANNVD 253  
Db 316 KVG-N-FVALRSTIORIOERK---IPALGTESSRSSSSSFQHEMSQGFSSALSMD 364

## RESULT 4

US-08-605-672-46  
Sequence 46, Application US/08605672  
Patent No. 5817515  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
APPLICANT: Van der Vieren, Monica  
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum  
STREET: 233 South Wacker Drive, 6300 Seear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/605,672  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1155 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-605-672-46

Query Match 9.6%; Score 166; DB 2; Length 1155;  
Best Local Similarity 28.2%; Pred. No. 3.4e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;  
QY 37 PACYV-GFDLYFILDKSGSV-LHWNNEIYFVEQLAHKFIISPOLMSFIVSTRGTITMK 94  
Db 144 PECQEQENDIAFLIDGSGSIDQSDFTQMDPVKALMGQLASTSTFSIMQYSNLIKHTHT 203  
QY 95 LTEDR-----EQIRQGLELQKVLPGCDTYMHGEFERASEQIYYENROGYRTA-SVIAL 148  
Db 204 FTEPKSSISPSQSLVDALVQLQ-----GLTYTASGIQKVKELFHSKNGARKSAKKILIVI 258  
QY 149 TDGELHEDLFYYSR--REANRSRDIGAIYVCVGD-FNE-TQLARI-----ADSKDHVF 199  
Db 259 TDGQFRPDLRYHVIPEAKA---GIRYALGVGDARFEPALQELNTIGSAPSQDHVF 315

QY 200 PVNDGFOALQGIHSHILKKSCEIILAAEPSTTCAGESQVAVVNGGFRHANNVD 253  
Db 316 KVG-N-FVALRSTIORIOERK---IPALGTESSRSSSSSFQHEMSQGFSSALSMD 364

## RESULT 5

US-08-482-293A-46  
Sequence 46, Application US/08482293A  
Patent No. 5831029  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
APPLICANT: Van der Vieren, Monica  
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum  
STREET: 233 South Wacker Drive, 6300 Seear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,293A  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1155 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-482-293A-46

Query Match 9.6%; Score 166; DB 2; Length 1155;  
Best Local Similarity 28.2%; Pred. No. 3.4e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;  
QY 37 PACYV-GFDLYFILDKSGSV-LHWNNEIYFVEQLAHKFIISPOLMSFIVSTRGTITMK 94  
Db 144 PECQEQENDIAFLIDGSGSIDQSDFTQMDPVKALMGQLASTSTFSIMQYSNLIKHTHT 203  
QY 95 LTEDR-----EQIRQGLELQKVLPGCDTYMHGEFERASEQIYYENROGYRTA-SVIAL 148  
Db 204 FTEPKSSISPSQSLVDALVQLQ-----GLTYTASGIQKVKELFHSKNGARKSAKKILIVI 258  
QY 149 TDGELHEDLFYYSR--REANRSRDIGAIYVCVGD-FNE-TQLARI-----ADSKDHVF 199  
Db 259 TDGQFRPDLRYHVIPEAKA---GIRYALGVGDARFEPALQELNTIGSAPSQDHVF 315  
QY 200 PVNDGFOALQGIHSHILKKSCEIILAAEPSTTCAGESQVAVVNGGFRHANNVD 253

Db 316 KVGK-FVALRSIORIOERK-----IPALIGTSSRSSSSFOHMSOEGFSSALSMD 364

RESULT 6  
US-08-943-363-46  
Sequence 46, Application US/08943363  
Patent No. 5837478  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
APPLICANT: Van der Vieren, Monica  
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Seat Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/943.363  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173.497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286.889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362.652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: William Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1155 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-943-363-46

Query Match 9.6%; Score 166; DB 2; Length 1155;  
Best Local Similarity 28.2%; Pred. No. 3.4e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

Qy 37 PACYG-GFDLYFLIDKSGSV-LHHMNEYVVEQLAHKFIISPOLRMSFIYSTGTITLMK 94  
Db 144 PECQGEMLDIAFLIDGSGSIDQSDPTQKDFVAKLMGQLASTSTSFSLMQSNILKTHFT 203  
Qy 95 LTEDR-----EQIRQGLELQKVLPGGDTYMHGFEFERSQIYYENRGYRTA-SVIAL 148  
Db 204 FTERFKSLSPQSLVDIAVQLQ-----GLTYTASGIQKVVLELFSKNGAKRSACKILIVI 258  
Qy 149 TDGELHEDLFFYSE--REANRSRDLAGIYVCVGYKD-FNE-TOLARI-----ADSKOHVF 199  
Db 259 TDGQKFRDPLRYHVHVAPEAKA---GIIRYALGVDAFREPTALQELNTTIGSAPSOHV 315  
Qy 200 PVNDGFOLGIIHSLKSCIEILAAEPSTICAGSEFOVVVNGNGRFRHANYD 253  
Db 316 KVGK-FVALRSIORIOERK-----IPALIGTSSRSSSSFOHMSOEGFSSALSMD 364

RESULT 7  
US-09-193-043-46  
Sequence 46, Application US/09193043  
Patent No. 6251395  
GENERAL INFORMATION:  
APPLICANT: Gallatin, Michael W.  
APPLICANT: Van der Vieren, Monica  
TITLE OF INVENTION: No. 6251395el Human 2  
FILE REFERENCE: 27866/35004  
CURRENT APPLICATION NUMBER: US/09/193.043  
PRIOR APPLICATION NUMBER: 1998-11-16  
EARLIER FILING DATE: 08/173.497  
EARLIER FILING DATE: 1993-12-23  
EARLIER APPLICATION NUMBER: 08/286.889  
EARLIER FILING DATE: 1994-08-05  
EARLIER APPLICATION NUMBER: 08/362.652  
EARLIER FILING DATE: 1994-12-21  
EARLIER APPLICATION NUMBER: 08/943.363  
EARLIER FILING DATE: 1997-10-03  
NUMBER OF SEQ ID NOS: 114  
SOFTWARE: Patentn Ver. 2.0  
SEQ ID NO 46  
LENGTH: 1155  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-193-043-46

Query Match 9.6%; Score 166; DB 3; Length 1155;  
Best Local Similarity 28.2%; Pred. No. 3.4e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

Qy 37 PACYG-GFDLYFLIDKSGSV-LHHMNEYVVEQLAHKFIISPOLRMSFIYSTGTITLMK 94  
Db 144 PECQGEMLDIAFLIDGSGSIDQSDPTQKDFVAKLMGQLASTSTSFSLMQSNILKTHFT 203  
Qy 95 LTEDR-----EQIRQGLELQKVLPGGDTYMHGFEFERSQIYYENRGYRTA-SVIAL 148  
Db 204 FTERFKSLSPQSLVDIAVQLQ-----GLTYTASGIQKVVLELFSKNGAKRSACKILIVI 258  
Qy 149 TDGELHEDLFFYSE--REANRSRDLAGIYVCVGYKD-FNE-TOLARI-----ADSKOHVF 199  
Db 259 TDGQKFRDPLRYHVHVAPEAKA---GIIRYALGVDAFREPTALQELNTTIGSAPSOHV 315  
Qy 200 PVNDGFOLGIIHSLKSCIEILAAEPSTICAGSEFOVVVNGNGRFRHANYD 253  
Db 316 KVGK-FVALRSIORIOERK-----IPALIGTSSRSSSSFOHMSOEGFSSALSMD 364

RESULT 8  
US-09-688-307A-46  
Sequence 46, Application US/09688307A  
Patent No. 6432404  
GENERAL INFORMATION:  
APPLICANT: Gallatin, Michael W.  
APPLICANT: Van der Vieren, Monica  
TITLE OF INVENTION: No. 6432404el Human Beta-2  
FILE REFERENCE: 27866/36646  
CURRENT APPLICATION NUMBER: US/09/688.307A  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: 09/193.043  
PRIOR FILING DATE: 1998-11-16  
PRIOR APPLICATION NUMBER: 08/605.672  
PRIOR FILING DATE: 1996-02-22  
PRIOR APPLICATION NUMBER: 08/173.497  
PRIOR FILING DATE: 1993-12-23  
PRIOR APPLICATION NUMBER: 08/286.889  
PRIOR FILING DATE: 1994-08-05  
PRIOR APPLICATION NUMBER: 08/362.652  
PRIOR FILING DATE: 1994-12-21  
PRIOR APPLICATION NUMBER: 08/943.363  
PRIOR FILING DATE: 1997-10-03

NUMBER OF SEQ ID NOS: 114  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 46  
 LENGTH: 1155  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-09-688-307A-46

Query Match 9.6%; Score 166; DB 4; Length 1155;  
 Best Local Similarity 28.2%; Pred. No. 3.4e-09;  
 Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYV-GPDLVFIILKSGSV-LHHNNEIYFVEQLAHKFIISPOLMSPIVSTRTGLMK 94  
 DB 144 PEPQOEMDIAPLIDSGSIDSDTOMKDFKALMGQLASTSTSPSLMOYSNLIKTHFT 203  
 QY 95 LTEDR-----EQIRGLELQVLPKGDVTYMEGFERASEQIYYENROGYRTA-SVIAL 148  
 DB 204 FTEFSSLSLPSGLVDALVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILLVI 258  
 QY 149 TDGELHEDLFFYSE--REANRSRDIGAIYVCVKD-FNE-TQLARI-----ADSKDHYF 199  
 DB 259 TDGQKFRPDLRYRHVYIPEAKA---GIIRYALGVDAFREPTALQELMTIGSAPQDHYF 315  
 QY 200 PVDGFOALQGIHSLKSCIEILAEPSITCAGESFOVVRNGFPHARVD 253  
 DB 316 KVGK-FVALRSIQROIQEK---IFALIGTSRSSSSFOHEMSQGFSSALSM 364

## RESULT 9

US-09-350-259-46  
 Sequence 46, Application US/09350259  
 Patent No. 6620915  
 GENERAL INFORMATION:  
 APPLICANT: Gallatin, Michael W.  
 APPLICANT: Van der Vieren, Monica  
 TITLE OF INVENTION: No. 6620915e1 Human 2  
 FILE REFERENCE: 27866/35004  
 CURRENT APPLICATION NUMBER: US/09/350,259  
 FILING DATE: 1999-07-08  
 EARLIER APPLICATION NUMBER: 09/193,043  
 EARLIER FILING DATE: 1998-11-16  
 EARLIER APPLICATION NUMBER: 08/113,497  
 EARLIER FILING DATE: 1993-12-23  
 EARLIER APPLICATION NUMBER: 08/286,889  
 EARLIER FILING DATE: 1994-08-05  
 EARLIER APPLICATION NUMBER: 08/362,652  
 EARLIER FILING DATE: 1994-12-21  
 EARLIER APPLICATION NUMBER: 08/943,363  
 EARLIER FILING DATE: 1997-10-03  
 NUMBER OF SEQ ID NOS: 114  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 46  
 LENGTH: 1155  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-09-350-259-46

Query Match 9.6%; Score 166; DB 4; Length 1155;  
 Best Local Similarity 28.2%; Pred. No. 3.4e-09;  
 Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYV-GPDLVFIILKSGSV-LHHNNEIYFVEQLAHKFIISPOLMSPIVSTRTGLMK 94  
 DB 144 PEPQOEMDIAPLIDSGSIDSDTOMKDFKALMGQLASTSTSPSLMOYSNLIKTHFT 203  
 QY 95 LTEDR-----EQIRGLELQVLPKGDVTYMEGFERASEQIYYENROGYRTA-SVIAL 148  
 DB 204 FTEFSSLSLPSGLVDALVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILLVI 258  
 QY 149 TDGELHEDLFFYSE--REANRSRDIGAIYVCVKD-FNE-TQLARI-----ADSKDHYF 199  
 DB 259 TDGQKFRPDLRYRHVYIPEAKA---GIIRYALGVDAFREPTALQELMTIGSAPQDHYF 315

QY 200 PVDGFOALQGIHSLKSCIEILAEPSITCAGESFOVVRNGFPHARVD 253  
 DB 316 KVGK-FVALRSIQROIQEK---IFALIGTSRSSSSFOHEMSQGFSSALSM 364

## RESULT 10

US-08-485-618-53  
 Sequence 53, Application US/08485618  
 Patent No. 5728533  
 GENERAL INFORMATION:  
 APPLICANT: Gallatin, W. Michael  
 APPLICANT: Van der Vieren, Monica  
 TITLE OF INVENTION: No. 5728533e1 Human 2 Integrin Alpha Subunit  
 NUMBER OF SEQUENCES: 103  
 CORRESPONDENCE ADDRESSES:  
 ADDRESS: Marshall, O'Toole, Gerstein, Murray & Bornun  
 STREET: 233 South Wacker Drive, 6300 Sear Tower  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: United States  
 ZIP: 60606-6402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/485,618  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/173,497  
 FILING DATE: 23-DEC-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/286,889  
 FILING DATE: 5-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/362,652  
 FILING DATE: 21-DEC-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Williams Jr., Joseph A.  
 REGISTRATION NUMBER: 38,659  
 REFERENCE/DOCKET NUMBER: 27866/32797  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312-474-6300  
 TELEFAX: 312-474-0448  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 53:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1161 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-485-618-53

Query Match 9.6%; Score 166; DB 1; Length 1161;  
 Best Local Similarity 28.2%; Pred. No. 3.4e-09;  
 Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYV-GPDLVFIILKSGSV-LHHNNEIYFVEQLAHKFIISPOLMSPIVSTRTGLMK 94  
 DB 144 PEPQOEMDIAPLIDSGSIDSDTOMKDFKALMGQLASTSTSPSLMOYSNLIKTHFT 203  
 QY 95 LTEDR-----EQIRGLELQVLPKGDVTYMEGFERASEQIYYENROGYRTA-SVIAL 148  
 DB 204 FTEFSSLSLPSGLVDALVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILLVI 258  
 QY 149 TDGELHEDLFFYSE--REANRSRDIGAIYVCVKD-FNE-TQLARI-----ADSKDHYF 199  
 DB 259 TDGQKFRPDLRYRHVYIPEAKA---GIIRYALGVDAFREPTALQELMTIGSAPQDHYF 315  
 QY 200 PVDGFOALQGIHSLKSCIEILAEPSITCAGESFOVVRNGFPHARVD 253

Db 316 KVG-N-FVALRSIQIOIEK-----IFAIGTESRSSSSFOHMSQEGFSSALSMD 364

## RESULT 11

US-08-362-652-53  
; Sequence 53, Application US/08362652  
; Patent No. 5766850  
; GENERAL INFORMATION:  
; APPLICANT: Gallatin, W. Michael  
; APPLICANT: Van der Vlieten, Monica  
; TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit  
; NUMBER OF SEQUENCES: 93  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 South Wacker Drive, 6300 Sear Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/362,652  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/173,497  
; FILING DATE: 23-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/286,889  
; FILING DATE: 5-AUG-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams Jr., Joseph A.  
; REGISTRATION NUMBER: 38,659  
; REFERENCE/DOCKET NUMBER: 27866/32391  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; TELEFAX: 312-474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1161 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-362-652-53

Query Match 9.6%; Score 166; DB 1; Length 1161;  
Best Local Similarity 28.2%; Pred. No. 3.4e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

Qy 37 PACYG-GPDLYFLIDKSGSV-LHMHNEIYFVEQLAHFISPOLMSEFIVSTGTILMK 94  
Db 144 PECGQEMDIAFLIDGSGSIDQSDFTQKDFVKALMGQLASTSTFSLMQYSNILKTHFT 203  
Qy 95 LTERD-----EQIQGLEBLQKVLPGSDTYMHGFERASEQIYYENRGYTA-SVITAL 148  
Db 204 FTEFKSLSPQSLDAIVQLQ-----GLYTTASGIQKVKELFHSKNGARKSAKKILIVI 258  
Qy 149 TDGELHDLFFYSE--REANRSRDGAIVYCVGVD-FNE-TQLARI-----ADSKDHVF 199  
Db 259 TDGQKFRDPLEYRHVYIEAEKA--GIRYALGVDAFREPTALQELNTIGSAPSQDHVF 315  
Qy 200 PVNDGFALQGIHSLKKSCEITLAAPSTICAGESFOVVVRGNGFRHARNVD 253  
Db 316 KVG-N-FVALRSIQIOIEK-----IFAIGTESRSSSSFOHMSQEGFSSALSMD 364

## RESULT 12

US-08-605-672-53  
; Sequence 53, Application US/08605672  
; Patent No. 5817515  
; GENERAL INFORMATION:  
; APPLICANT: Gallatin, W. Michael  
; APPLICANT: Van der Vlieten, Monica  
; TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 South Wacker Drive, 6300 Sear Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/605,672  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/173,497  
; FILING DATE: 23-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/286,889  
; FILING DATE: 5-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/362,652  
; FILING DATE: 21-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams Jr., Joseph A.  
; REGISTRATION NUMBER: 38,659  
; REFERENCE/DOCKET NUMBER: 27866/32684  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; TELEFAX: 312-474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1161 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-605-672-53

Query Match 9.6%; Score 166; DB 2; Length 1161;  
Best Local Similarity 28.2%; Pred. No. 3.4e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

Qy 37 PACYG-GPDLYFLIDKSGSV-LHMHNEIYFVEQLAHFISPOLMSEFIVSTGTILMK 94  
Db 144 PECGQEMDIAFLIDGSGSIDQSDFTQKDFVKALMGQLASTSTFSLMQYSNILKTHFT 203  
Qy 95 LTERD-----EQIQGLEBLQKVLPGSDTYMHGFERASEQIYYENRGYTA-SVITAL 148  
Db 204 FTEFKSLSPQSLDAIVQLQ-----GLYTTASGIQKVKELFHSKNGARKSAKKILIVI 258  
Qy 149 TDGELHDLFFYSE--REANRSRDGAIVYCVGVD-FNE-TQLARI-----ADSKDHVF 199  
Db 259 TDGQKFRDPLEYRHVYIEAEKA--GIRYALGVDAFREPTALQELNTIGSAPSQDHVF 315  
Qy 200 PVNDGFALQGIHSLKKSCEITLAAPSTICAGESFOVVVRGNGFRHARNVD 253  
Db 316 KVG-N-FVALRSIQIOIEK-----IFAIGTESRSSSSFOHMSQEGFSSALSMD 364

RESULT 13  
US-08-482-293A-53  
; Sequence 53, Application US/08482293A

Patent No. 5831029  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
APPLICANT: Van der Vieren, Monica  
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Sear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,293A  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1161 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-482-293A-53

Query Match 9.6%; Score 166; DB 2; Length 1161;  
Best Local Similarity 28.2%; Pred. No. 3.4e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACTG-GPDLYFLDKSGSV-LHNNELIYFVEQLAHKFIISPOLMSFIVSTRTITLMK 94  
DB 144 PECPOENDIADFLDGSISIDQSDPTQKDFKALMGQLASTSTFSIMQYSNILKHT 203  
QY 95 LTEDR-----EQIRGLELQVLPQGDITYHEGFERASEQIYENRQGYRTA-SVITAL 148  
DB 204 FTEFKSSISPSGLVDALVOLQ-----GLTYTASGIQKVKELFHSKNGARKSAKILIVI 258  
QY 149 TDGELHEDLFFYSR--REANRSRDGAIVYCVGVD-FNE-TQLARI-----ADSKDHYF 199  
DB 259 TDGQFRDPLERHYIPEAKA---GIIRYAIQVDGDAFREPALQELNTIGSAPQDHYF 315  
QY 200 PYNDGFQALQGIHSLKKSCEILAAEPSTICAGESFQVVRGNGFRRHARVD 253  
DB 316 KVG-N-FVALRSIQRIQERK---IFALIGTESRSSSSFQHEMSQGFSSALSMD 364

RESULT 14  
US-08-943-363-53  
Sequence 53, Application US/08943363  
Patent No. 5837478  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael

APPLICANT: Gallatin, W. Michael  
APPLICANT: Van der Vieren, Monica  
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Sear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,363  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1161 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-943-363-53

Query Match 9.6%; Score 166; DB 2; Length 1161;  
Best Local Similarity 28.2%; Pred. No. 3.4e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACTG-GPDLYFLDKSGSV-LHNNELIYFVEQLAHKFIISPOLMSFIVSTRTITLMK 94  
DB 144 PECPOENDIADFLDGSISIDQSDPTQKDFKALMGQLASTSTFSIMQYSNILKHT 203  
QY 95 LTEDR-----EQIRGLELQVLPQGDITYHEGFERASEQIYENRQGYRTA-SVITAL 148  
DB 204 FTEFKSSISPSGLVDALVOLQ-----GLTYTASGIQKVKELFHSKNGARKSAKILIVI 258  
QY 149 TDGELHEDLFFYSR--REANRSRDGAIVYCVGVD-FNE-TQLARI-----ADSKDHYF 199  
DB 259 TDGQFRDPLERHYIPEAKA---GIIRYAIQVDGDAFREPALQELNTIGSAPQDHYF 315  
QY 200 PYNDGFQALQGIHSLKKSCEILAAEPSTICAGESFQVVRGNGFRRHARVD 253  
DB 316 KVG-N-FVALRSIQRIQERK---IFALIGTESRSSSSFQHEMSQGFSSALSMD 364

RESULT 15  
US-09-193-043-53  
Sequence 53, Application US/09193043  
Patent No. 6251395  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
APPLICANT: Van der Vieren, Monica



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 21, 2004, 13:39:51 / Search time 21.2974 Seconds

(without alignment)  
1367.166 Million cell updates/sec

Title: US-09-970-076-6

Perfect score: 3025

Sequence: 1 MATERRALGICFQWLSLAT.....QAPPNNRAPPPSPRRPSV 564

Scoring table:

BLOSUM62

Gapop 10.0 / Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/prodata/2/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/prodata/2/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/prodata/2/1aa/6CTUS\_COMB.pep:\*
- 6: /cgn2\_6/prodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	199	6.6	104	US-09-547-693-235	Sequence 235, App1
2	191.5	6.3	306	US-08-217-327-6	Sequence 6, App1
3	186	6.1	76	US-09-547-693-233	Sequence 233, App1
4	186	6.1	214	US-08-217-327-4	Sequence 4, App1
5	173.5	5.7	142	US-09-252-991A-24873	Sequence 24873, A
6	173.5	5.7	334	US-09-252-991A-24873	Sequence 24873, A
7	171.5	5.7	331	US-09-252-991A-24873	Sequence 24873, A
8	167.5	5.5	1248	US-09-080-897-2	Sequence 2, App1
9	167.5	5.5	1248	US-09-323-735-2	Sequence 2, App1
10	167	5.5	1231	US-08-714-741-41	Sequence 41, App1
11	166	5.5	1155	US-08-286-889-46	Sequence 46, App1
12	166	5.5	1155	US-08-485-618-46	Sequence 46, App1
13	166	5.5	1155	US-08-362-652-46	Sequence 46, App1
14	166	5.5	1155	US-08-605-672-46	Sequence 46, App1
15	166	5.5	1155	US-08-482-293A-46	Sequence 46, App1
16	166	5.5	1155	US-08-943-363-46	Sequence 46, App1
17	166	5.5	1155	US-09-193-043-46	Sequence 46, App1
18	166	5.5	1155	US-09-688-307A-46	Sequence 46, App1
19	166	5.5	1155	US-09-350-259-46	Sequence 46, App1
20	166	5.5	1161	US-08-485-618-53	Sequence 53, App1
21	166	5.5	1161	US-08-362-652-53	Sequence 53, App1
22	166	5.5	1161	US-08-605-672-53	Sequence 53, App1
23	166	5.5	1161	US-08-482-293A-53	Sequence 53, App1
24	166	5.5	1161	US-08-943-363-53	Sequence 53, App1
25	166	5.5	1161	US-09-193-043-53	Sequence 53, App1
26	166	5.5	1161	US-09-688-307A-53	Sequence 53, App1
27	166	5.5	1161	US-09-350-259-53	Sequence 53, App1

28	165	5.5	105	US-09-547-693-230	Sequence 230, App1
29	163	5.4	635	US-07-833-855-2	Sequence 2, App1
30	162.5	5.4	203	US-09-543-681A-8287	Sequence 8287, App1
31	162	5.4	559	US-10-116-370-2	Sequence 2, App1
32	161.5	5.3	1315	US-08-899-595-3	Sequence 3, App1
33	161	5.3	72	US-09-547-693-231	Sequence 231, App1
34	160.5	5.3	1255	US-09-080-897-4	Sequence 4, App1
35	160.5	5.3	1255	US-08-899-595-1	Sequence 1, App1
36	160.5	5.3	1255	US-09-323-735-4	Sequence 4, App1
37	159.5	5.3	503	US-09-599-287A-2	Sequence 2, App1
38	159.5	5.3	1151	US-08-286-889-37	Sequence 37, App1
39	159.5	5.3	1151	US-08-485-618-37	Sequence 37, App1
40	159.5	5.3	1151	US-08-362-652-37	Sequence 37, App1
41	159.5	5.3	1151	US-08-605-672-37	Sequence 37, App1
42	159.5	5.3	1151	US-08-482-293A-37	Sequence 37, App1
43	159.5	5.3	1151	US-08-943-363-37	Sequence 37, App1
44	159.5	5.3	1151	US-09-193-043-37	Sequence 37, App1
45	159.5	5.3	1151	US-09-688-307A-37	Sequence 37, App1

#### ALIGNMENTS

RESULT 1  
US-09-547-693-235  
Sequence 235, Application US/09547693  
Patent No. 6639050  
GENERAL INFORMATION:  
APPLICANT: Kleiszewski, Marcia  
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich  
FILE REFERENCE: OHU-04089  
CURRENT APPLICATION NUMBER: US/09/547,693  
CURRENT FILING DATE: 2000-04-12  
NUMBER OF SEQ ID NOS: 236  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 235  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Artificial/Unknown  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Synthetic  
US-09-547-693-235

Query Match 6.6%; Score 199; DB 4; Length 104;  
Best Local Similarity 47.5%; Pred. No. 4.2e-10;  
Matches 38; Conservative 7; Mismatches 33; Indels 2; Gaps 1;

QY 485 TRVKNQPAKTYLNNAYHTSSPPAPITPPPPHCPPPPSAFTPPSPSTLP--P 542  
DB 4 TRASPPSP 63  
543 PPOAPPNNRAPPPSPRRPP 562  
64 PPSPPSPSPSPSPSPSPSP 83

RESULT 2  
US-08-217-327-6  
Sequence 6, Application US/08217327  
Patent No. 5474925  
GENERAL INFORMATION:  
APPLICANT: John, Maliyakal E  
TITLE OF INVENTION: Barton, Kenneth A  
TITLE OF INVENTION: Immobilized Proteins in Cotton Fiber  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: Quarles and Brady  
STREET: P.O. Box 2113  
CITY: Madison  
STATE: WI  
COUNTRY: USA

ZIP: 53701-2113  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/217,327  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/812,233  
 FILING DATE: 19-DEC-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seay, Nicholas J  
 REGISTRATION NUMBER: 27,386  
 REFERENCE/DOCKET NUMBER: 1122990831  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 608-251-5000  
 TELEFAX: 608-251-9166  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 306 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-217-327-6

Query Match 6.3%; Score 191.5; DB 1; Length 306;  
 Best Local Similarity 26.1%; Pred. No. 9e-09;  
 Matches 59; Conservative 18; Mismatches 56; Indels 93; Gaps 10;

352 KEVPP---PAEESSEEDDDGLPKKQWPTVDASYGGRGVGIGIKMEVMEKSTEGGA 408  
 144 KSPPPKSPAPENHYTKKSPPPKHPAPENHY----- 177  
 409 KLEKAKNARYVMEQGEYFPEPRRLNNMRRSPSPKWSPIKGLDALWVLRKGYDRV 468  
 178 -KYKKSPPPPTPVYKKSP-----PTPVYKKSP----- 208  
 469 SVMRQPDGTGRCLNFTVKNNQPAKYPLNNAHYTSSPPAPITYPPAPHCPPPP-- 526  
 209 ---PPP-----KSPAP--PVNHKKYKSPPPPTPVYKSPPPPHSPPPPTPV 249  
 527 ---SAPTPPIPSPTLPPPP-----QAPPRAPPP--GRPPR 561  
 250 YKYSPPPPMHSPP--PPTPVYKYSPPPPMHSPPPPVYSPPPPK 292  
 Db

RESULT 3  
 US-09-547-693-233  
 Sequence 233, Application US/09547693  
 Patent No. 6639050  
 GENERAL INFORMATION:  
 APPLICANT: Kieliszewski, Marcia  
 TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich  
 TITLE OF INVENTION: Glycoproteins  
 FILE REFERENCE: OHU-04089  
 CURRENT APPLICATION NUMBER: US/09/547,693  
 CURRENT FILING DATE: 2000-04-12  
 NUMBER OF SEQ ID NOS: 236  
 SOFTWARE: Patentin version 3.0  
 SEQ ID NO 233  
 LENGTH: 76  
 TYPE: PRT  
 ORGANISM: Artificial/Unknown  
 FEATURE:  
 NAME/KEY: misc feature  
 OTHER INFORMATION: Synthetic  
 US-09-547-693-233

Query Match 6.1%; Score 186; DB 4; Length 76;  
 Best Local Similarity 56.2%; Pred. No. 3.7e-09;

Matches 36; Conservative 6; Mismatches 18; Indels 4; Gaps 3;  
 505 SPPAPITYPPAPAPHCPP--PPSAPTPPIPSPTLPP--PPOAPPPNAP--PPSAPP 560  
 12 SPPSP 71  
 561 RPSV 564  
 72 SPSM 75  
 Db

RESULT 4  
 US-08-217-327-4  
 Sequence 4, Application US/08217327  
 Patent No. 5474925  
 GENERAL INFORMATION:  
 APPLICANT: John, Mallyakal E  
 APPLICANT: Barton, Kenneth A  
 TITLE OF INVENTION: Immobilized Proteins in Cotton Fiber  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Charles and Brady  
 STREET: P.O. Box 2113  
 CITY: Madison  
 STATE: WI  
 COUNTRY: USA  
 ZIP: 53701-2113  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/217,327  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/812,233  
 FILING DATE: 19-DEC-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seay, Nicholas J  
 REGISTRATION NUMBER: 27,386  
 REFERENCE/DOCKET NUMBER: 1122990831  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 608-251-5000  
 TELEFAX: 608-251-9166  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 214 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-217-327-4

Query Match 6.1%; Score 186; DB 1; Length 214;  
 Best Local Similarity 47.0%; Pred. No. 1.7e-08;  
 Matches 39; Conservative 5; Mismatches 23; Indels 16; Gaps 4;

496 PLNNAHYTSSPPA-----PIYTPPP--PAVHCPP--PPSAPTPPIPSPTLPP----- 542  
 60 PVSTRPPTSSPPPTVSP 119  
 543 ---PPOAPPPNAPPPSPPPPP 562  
 120 PATPPATPPATPPATPPPPAP 142  
 Db

RESULT 5  
 US-09-252-991A-24873  
 Sequence 24873, Application US/09252991A  
 Patent No. 6551795  
 GENERAL INFORMATION:  
 APPLICANT: Marc J. Rubenfield et al.



TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 24873  
LENGTH: 142  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-24873

Query Match 5.7%; Score 173.5; DB 4; Length 142;  
Best Local Similarity 53.7%; Pred. No. 1.2e-07;  
Matches 36; Conservative 7; Mismatches 15; Indels 9; Gaps 5;

QY 506 PPAPITPPPPAPHCPPP---PPSAFTPTPI-PSPESTLPP-PQADPPNRP--PPSR 557  
Db 66 PPPSPSPSPPPVPVPPSPVPPVPPSPPPVPPSPPPVPPSPPPVPPSPPPVPPSP 125

QY 558 P-PPRPS 563  
Db 126 PGPPSPS 132

RESULT 6  
5202236-3  
PATENT NO. 5202236  
APPLICANT: MUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG,  
SUSAN L.; MCCANDLIS, RUSSELL; TENA, FILIPULA, DAVID  
TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE  
PROTEIN  
NUMBER OF SEQUENCES: 39  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/528,762  
FILING DATE: 25-MAY-1990  
APPLICATION NUMBER: 82,456  
FILING DATE: 07-AUG-1987  
APPLICATION NUMBER: 933,945  
FILING DATE: 24-NOV-1986  
APPLICATION NUMBER: 650,128  
FILING DATE: 13-SEP-1984  
SEQ ID NO: 3  
LENGTH: 334  
5202236-3

Query Match 5.7%; Score 173.5; DB 6; Length 334;  
Best Local Similarity 51.6%; Pred. No. 4e-07;  
Matches 33; Conservative 4; Mismatches 16; Indels 11; Gaps 3;

QY 507 PPAPITPPPP-----PAPHCPPPPPSAPTPPIPSPESTLPPPPQADPPNRP--PPSR 558  
Db 8 PPAPAFAPALAPAPNPVPPSPSPSPPTTP--PPAPSPSPSPSPVPPSP 64

QY 559 PPRP 562  
Db 65 PPSP 68

RESULT 7  
5202236-37  
PATENT NO. 5202236  
APPLICANT: MUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG,  
SUSAN L.; MCCANDLIS, RUSSELL; TENA, FILIPULA, DAVID  
TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE  
PROTEIN  
NUMBER OF SEQUENCES: 39  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/528,762

FILING DATE: 25-MAY-1990  
APPLICATION NUMBER: 82,456  
FILING DATE: 07-AUG-1987  
APPLICATION NUMBER: 933,945  
FILING DATE: 24-NOV-1986  
APPLICATION NUMBER: 650,128  
FILING DATE: 13-SEP-1984  
SEQ ID NO: 37  
LENGTH: 331  
5202236-37

Query Match 5.7%; Score 171.5; DB 6; Length 331;  
Best Local Similarity 51.6%; Pred. No. 5.9e-07;  
Matches 33; Conservative 4; Mismatches 16; Indels 11; Gaps 3;

QY 507 PPAPITPPPP-----PAPHCPPPPPSAPTPPIPSPESTLPPPPQADPPNRP--PPSR 558  
Db 5 PPAPAFAPALAPAPNPVPPSPSPSPPTTP--PPAPSPSPSPSPVPPSP 61

QY 559 PPRP 562  
Db 62 PPSP 65

RESULT 8  
US-09-080-897-2  
Sequence 2, Application US/09080897  
PATENT NO. 5985574  
GENERAL INFORMATION:  
APPLICANT: King, Mary-Claire  
APPLICANT: Lynch, Eric D.  
APPLICANT: Lee, Ming  
APPLICANT: Morrow, Jan E.  
APPLICANT: Welch, Piri L.  
APPLICANT: Leon, Pedro E.  
TITLE OF INVENTION: Modulators of Actin  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 75 DENISE DRIVE  
CITY: HILLSBOROUGH  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94010  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/080,897  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A.  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: 0997-001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-4341  
TELEFAX: (650) 343-4342  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1248 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-080-897-2

Query Match 5.5%; Score 167.5; DB 2; Length 1248;  
Best Local Similarity 35.5%; Pred. No. 9e-06;  
Matches 43; Conservative 3; Mismatches 20; Indels 55; Gaps 6;

QY 473 PQPDGTGRCINFTVKNQNPAPKYPLNNAVHTSSPPAP--IYTPPPAPHCPPPP----- 526

Db 578 PLPGDSGTRI-----PPPPAGDSTPPPPPPPPPPPLGCG 615  
Qy 527 -----SAPRP-----IPSPS-----TLPPEQAAPPNAPPSRPPR 561  
Db 616 TAIAPPPLSGDATIPPPPLPEGVGIRPSGLPGCTAIPPPPLPSGARIPPP--PPPL 673  
Qy 562 P 562  
Db 674 P 674

RESULT 9  
US-09-323-735-2  
Sequence 2, Application US/09323735  
Patent No. 6197932  
GENERAL INFORMATION:  
APPLICANT: King, Mary-Claire  
APPLICANT: Lynch, Eric D.  
APPLICANT: Lee, Ming  
APPLICANT: Morrow, Jan E.  
APPLICANT: Welch, Birt L.  
APPLICANT: Leon, Pedro E.  
TITLE OF INVENTION: Modulators of Actin  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 75 DENISE DRIVE  
CITY: HILLSBOROUGH  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94010  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/323,735  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/080,897  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: UM97-001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-4341  
TELEFAX: (650) 343-4342  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1248 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-323-735-2

Query Match 5.5%; Score 167.5; DB 3; Length 1248;  
Best Local Similarity 35.5%; Pred. No. 9e-06;  
Matches 43; Conservative 3; Mismatches 20; Indels 55; Gaps 6;

Qy 473 POPGDTGRCINFRKNNQAPKYPLNNAYHTSSPPAP--ITYPPPAHCPPPPP----- 526  
Db 578 PLPGDSGTRI-----PPPPAGDSTPPPPPPPPPPPLGCG 615  
Qy 527 -----SAPRP-----IPSPS-----TLPPEQAAPPNAPPSRPPR 561  
Db 616 TAIAPPPLSGDATIPPPPLPEGVGIRPSGLPGCTAIPPPPLPSGARIPPP--PPPL 673  
Qy 562 P 562

Db 674 P 674

RESULT 10  
US-08-714-741-41  
Sequence 41, Application US/08714741  
Patent No. 6500613  
GENERAL INFORMATION:  
APPLICANT: Briles, David E.  
APPLICANT: McDaniel, Larry S.  
APPLICANT: Swiatlo, Edwin  
APPLICANT: Yotner, Janet  
APPLICANT: Crain, Marilyn J.  
APPLICANT: Hollingshead, Susan  
APPLICANT: Tart, Rebecca  
APPLICANT: Brooks-Walter, Alexis  
TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,  
TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,  
TITLE OF INVENTION: PORTIONS AND PRODUCTS  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Curtis, Morris & Safford, P.C.  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/714,741  
FILING DATE: 16-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer Esq., William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454312-2460  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1231 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: amino acid  
US-08-714-741-41

Query Match 5.5%; Score 167; DB 4; Length 1231;  
Best Local Similarity 31.4%; Pred. No. 9.8e-06;  
Matches 54; Conservative 16; Mismatches 72; Indels 30; Gaps 7;

Qy 400 EKSGTEGAKLEKAKNARVQKPEQVEFPPEP-----RNLNNMR--PSSPRKYSPKIG 452  
Db 565 EKTAEKKALEKAE-ADLKAVDEPPTAPAPQKAEENNNVEDYKKEGKTIKAKKA 623  
Qy 453 KLDALWTLRLKKYDRVSMRPPQDGTGRCINFRKNNQAPKYPLNNAYHTSSPPAPYI 512  
Db 624 ELEKTEADLKAVVEPEKPAAP-----EPAPAEKDA---EKPAAP-- 663  
Qy 513 TTPPPAHCPPPPSAPTPPIPS--PSTLPPPAQAPPNAPPSRPPPP 562  
Db 664 EKPAAPAEKPAAPAEKPAAPATPAEAPAEQPKAPAPQAPAPAEKPAAP 715

RESULT 11  
US-08-286-889-46  
Sequence 46, Application US/08286889  
Patent No. 5470953

GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Mich  
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Sear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/286,889  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: P38,659  
REFERENCE/DOCKET NUMBER: 27866/32168  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1155 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-286-889-46

Query Match 5.5%; Score 166; DB 1; Length 1155;  
Best Local Similarity 28.2%; Pred. No. 1.1e-05;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYV-GFDLYFLIDKSGSV-LHNNELIYFVEQLAHFISPOLMSFIVSTRGTTLMK 94  
DB 144 PECQEQEMDIAPFLIDGSGSIDQSDPTQMKDFVKALMGQLASTSTSFSLMOYSNLIKTHFT 203  
QY 95 LTEDR-----EQIRQGLELQKVLPGDPTVMHEGFERASEQIYYENRCGYRTA-SVITL 148  
DB 204 FTEFSSLSLPSQSLVDALVQLQ-----GLTYTASGIQKVKELFHSKNGARKSAKKILIVI 258  
QY 149 TDGELHEDLFFYSR--REANRSRDIGAIYVCVKD-FNE-TQLARI-----ADSKDHYF 199  
DB 259 TDGQKFRDPLRYRHVYPAEKRA---GIRYAVIGVDARFEPALQELMTIGSAPSDHYF 315  
QY 200 PVNDGFOLQGIHSLKKSCEILAAEPSTICAGESFQVVRVNGGFRHARNVD 253  
DB 316 KVG-N-FVALRSIORIOEK---IFAIGTESRSSSFQHEWSQGFSSALSMD 364

RESULT 12  
US-08-485-618-46  
Sequence 46, Application US/08485618  
Patent No. 5728533  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Sear Tower  
CITY: Chicago  
STATE: Illinois

CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,618  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32797  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1155 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-485-618-46

Query Match 5.5%; Score 166; DB 1; Length 1155;  
Best Local Similarity 28.2%; Pred. No. 1.1e-05;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYV-GFDLYFLIDKSGSV-LHNNELIYFVEQLAHFISPOLMSFIVSTRGTTLMK 94  
DB 144 PECQEQEMDIAPFLIDGSGSIDQSDPTQMKDFVKALMGQLASTSTSFSLMOYSNLIKTHFT 203  
QY 95 LTEDR-----EQIRQGLELQKVLPGDPTVMHEGFERASEQIYYENRCGYRTA-SVITL 148  
DB 204 FTEFSSLSLPSQSLVDALVQLQ-----GLTYTASGIQKVKELFHSKNGARKSAKKILIVI 258  
QY 149 TDGELHEDLFFYSR--REANRSRDIGAIYVCVKD-FNE-TQLARI-----ADSKDHYF 199  
DB 259 TDGQKFRDPLRYRHVYPAEKRA---GIRYAVIGVDARFEPALQELMTIGSAPSDHYF 315  
QY 200 PVNDGFOLQGIHSLKKSCEILAAEPSTICAGESFQVVRVNGGFRHARNVD 253  
DB 316 KVG-N-FVALRSIORIOEK---IFAIGTESRSSSFQHEWSQGFSSALSMD 364

RESULT 13  
US-08-362-652-46  
Sequence 46, Application US/08362652  
Patent No. 5766850  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Sear Tower  
CITY: Chicago  
STATE: Illinois

COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,652  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32391  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1155 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-362-652-46

Query Match 5.5%; Score 166; DB 1; Length 1155;  
Best Local Similarity 28.2%; Pred. No. 1.1e-05;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;  
QY 37 PACYG-GPDIYFIIDKSGSV-LHHMNEIYFVEQLAHKFIISPOLRMSPIVSTRTGLMK 94  
DB 144 PECGQEMDIAPFLIDGSGSIDQSDPTQMKDFVKALMGQLASTSTSPSLMOYSNLKTHFT 203  
QY 95 LTERD-----EQIRGLEELQKVLPGGDTYMHGFEKRSQIYYENRGYRTA-SVIAL 148  
DB 204 FTERKSLSPQSLDAIVQLQ-----GLTYTASGIQKVKELFHSKNGARKSACKILIVI 258  
QY 149 TDGELHEDLFYYSR--REANRSRLGAIYVCVGVKD-FNE-TOLARI-----ADSKDHF 199  
DB 259 TDGQKRPDLPEYHNVIPAERKA---GIRYALGVGDARFEPYALQELNTTGSAPSQDHVF 315  
QY 200 PVNDGFQALQGIHSLKSCIEILAEPSITCAGESFOVYVVRGNGFRHARNVD 253  
DB 316 KVGK-FVALRSIQROIQEK---IFAIEGTESRSSSFQHEMSQEGFSALSMD 364

RESULT 14  
US-08-605-672-46  
Sequence 46, Application US/08605672  
Patent No. 5817515  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
APPLICANT: Van der Vlieten, Monica  
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Sear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/605,672  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1155 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-605-672-46

Query Match 5.5%; Score 166; DB 2; Length 1155;  
Best Local Similarity 28.2%; Pred. No. 1.1e-05;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;  
QY 37 PACYG-GPDIYFIIDKSGSV-LHHMNEIYFVEQLAHKFIISPOLRMSPIVSTRTGLMK 94  
DB 144 PECGQEMDIAPFLIDGSGSIDQSDPTQMKDFVKALMGQLASTSTSPSLMOYSNLKTHFT 203  
QY 95 LTERD-----EQIRGLEELQKVLPGGDTYMHGFEKRSQIYYENRGYRTA-SVIAL 148  
DB 204 FTERKSLSPQSLDAIVQLQ-----GLTYTASGIQKVKELFHSKNGARKSACKILIVI 258  
QY 149 TDGELHEDLFYYSR--REANRSRLGAIYVCVGVKD-FNE-TOLARI-----ADSKDHF 199  
DB 259 TDGQKRPDLPEYHNVIPAERKA---GIRYALGVGDARFEPYALQELNTTGSAPSQDHVF 315  
QY 200 PVNDGFQALQGIHSLKSCIEILAEPSITCAGESFOVYVVRGNGFRHARNVD 253  
DB 316 KVGK-FVALRSIQROIQEK---IFAIEGTESRSSSFQHEMSQEGFSALSMD 364

RESULT 15  
US-08-482-293A-46  
Sequence 46, Application US/08482293A  
Patent No. 5831029  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
APPLICANT: Van der Vlieten, Monica  
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Sear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,293A  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1155 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-482-293A-46

Query Match 5.5%; Score 166; DB 2; Length 1155;  
Best Local Similarity 28.2%; Pred. No. 1.1e-05;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

OY 37 PACTG-GFDLFIIDKSGSV-LHWNIEIYFVEQLAHKFIISPOLMSPIVSTGTTLMK 94  
DB 144 PECFQEMDIAPFLIDSGSIDQSDFTQMKDFVKALMGQLASTSTSPSLMOYSNLIKTHFT 203  
OY 95 LTEDR-----EQIRGLELQKVLPGDPTMHGEPERASEQIYYENRQGYRTA-SVITL 148  
DB 204 FTERKSSLSPOSVDATVQLQ-----GLYTAGIGIQVVKELFHSKNGARKSAKKILIVT 258  
OY 149 TDGELHEDLFPYSE--REANRSRLDAIVYCVVD-FNE--TOLARI-----ADSKDHF 199  
DB 259 TDGQKFRDPLEYRHVYIPEAEKA---GIRVAIGVGDAFREPTALQELNTIGSAPSQDHF 315  
OY 200 PVNDGFALQGIHISILKKSCTEIIAABSTICAGESFQVVRNGGFRHARNVD 253  
DB 316 KVGN-FVALRSIQRIQIEK---IPALGTESRSSSSFOHEMSQEGFSSALSM 364

Search completed: June 21, 2004, 13:46:35  
Job time : 22.2974 secs

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GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 22, 2004, 02:37:46 ; Search time 840.105 Seconds

(without alignment)

3075.489 Million cell updates/sec

Title: US-09-970-076-6  
Perfect score: 3025  
Sequence: 1 MATERRALGICGFWLSLST.....QAPENRAPPSRPPRPSV 564

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-Q=/cgn2\_1/USPFO\_epool/US09970076/runac\_21062004.125533.8805/app\_query.fasta\_1.2140  
-DB=Published Applications NA -QPM=fastcap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPEL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blowsum62  
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=spc -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=100000000 -USER=US09970076\_@CGN\_1.1.1225\_@runac\_21062004.125533.8805  
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## Database :

Published Applications NA:  
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3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
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14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*  
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19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
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1	3025	100.0	5540	13	US-09-918-715-176	Sequence 176, App
2	3025	100.0	5540	13	US-09-918-715-231	Sequence 231, App
3	3025	100.0	5540	15	US-10-301-822-198	Sequence 198, App
4	2901	95.9	5220	13	US-09-918-715-186	Sequence 186, App
5	2901	95.9	5220	13	US-09-918-715-300	Sequence 300, App
6	2022	66.8	3981	13	US-10-302-172-250	Sequence 250, App
7	2017	66.7	4417	10	US-09-796-753-23	Sequence 23, Appl
8	2017	66.7	4417	15	US-10-038-307-3	Sequence 3, Appl
9	2017	66.7	4417	15	US-10-201-292-3	Sequence 3, Appl
10	1894	62.6	1454	16	US-10-133-337-58	Sequence 38, Appl
11	1894	62.6	1454	16	US-10-159-563-58	Sequence 58, Appl
12	1661	54.9	1674	15	US-10-038-307-17	Sequence 17, Appl
13	1661	54.9	1674	15	US-10-201-292-17	Sequence 17, Appl
14	1652.5	54.6	1650	15	US-10-038-307-15	Sequence 15, Appl
15	1652.5	54.6	1650	15	US-10-201-292-15	Sequence 15, Appl
16	1650.5	54.6	1650	15	US-10-038-307-13	Sequence 13, Appl
17	1650.5	54.6	1650	15	US-10-201-292-13	Sequence 13, Appl
18	1650	54.5	2272	10	US-09-796-753-11	Sequence 11, Appl
19	1650	54.5	2272	15	US-10-038-307-1	Sequence 1, Appl
20	1650	54.5	2272	15	US-10-201-292-1	Sequence 1, Appl
21	1650	54.5	2353	15	US-10-198-846-9957	Sequence 9957, App
22	1650	54.5	2459	9	US-09-833-381-998	Sequence 998, App
23	1649	54.5	1056	15	US-10-038-307-23	Sequence 23, Appl
24	1649	54.5	1056	15	US-10-201-292-23	Sequence 23, Appl
25	1649	54.5	1056	15	US-10-038-307-19	Sequence 19, Appl
26	1649	54.5	1713	15	US-10-201-292-19	Sequence 19, Appl
27	1640.5	54.2	1650	15	US-10-038-307-9	Sequence 9, Appl
28	1640.5	54.2	1650	15	US-10-201-292-9	Sequence 9, Appl
29	1636	54.1	1008	15	US-10-038-307-25	Sequence 25, Appl
30	1636	54.1	1008	15	US-10-201-292-25	Sequence 25, Appl
31	1634.5	54.0	1047	15	US-10-038-307-21	Sequence 21, Appl
32	1634.5	54.0	1047	15	US-10-201-292-21	Sequence 21, Appl
33	1557.5	51.5	1608	15	US-10-201-292-35	Sequence 35, Appl
34	1530	50.6	2397	16	US-10-062-674-1757	Sequence 1757, App
35	1509.5	49.9	1623	15	US-10-038-307-11	Sequence 11, Appl
36	1509.5	49.9	1623	15	US-10-201-292-11	Sequence 11, Appl
37	1423	47.0	2334	15	US-10-201-292-33	Sequence 33, Appl
38	1416.5	46.8	2234	16	US-10-104-047-669	Sequence 669, App
39	1416.5	46.8	4081	15	US-10-368-087-9	Sequence 9, Appl
40	1411.5	46.7	3677	10	US-09-796-753-51	Sequence 51, Appl
41	1411.5	46.7	3677	15	US-10-038-307-5	Sequence 5, Appl
42	1411.5	46.7	3677	15	US-10-201-292-5	Sequence 5, Appl
43	1411.5	46.7	4348	10	US-09-814-353-22000	Sequence 22000, A
44	1396.5	46.2	3501	10	US-09-796-753-53	Sequence 53, Appl
45	1396.5	46.2	3501	15	US-10-038-307-7	Sequence 7, Appl

## ALIGNMENTS

RESULT 1  
US-09-918-715-176  
; Sequence 176, Application US/09918715  
; Publication No. US20030017157A1  
GENERAL INFORMATION:  
APPLICANT: Brad St. Croix  
APPLICANT: Bert Vogelstein  
APPLICANT: Kenneth Kinzler  
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
FILE REFERENCE: 1107.00134  
CURRENT APPLICATION NUMBER: US/09/918,715  
CURRENT FILING DATE: 2001-08-01  
PRIOR APPLICATION NUMBER: 60/222,599  
PRIOR FILING DATE: 2000-08-02  
PRIOR APPLICATION NUMBER: 60/224,360  
PRIOR FILING DATE: 2000-08-11  
PRIOR APPLICATION NUMBER: 60/282,850  
PRIOR FILING DATE: 2000-04-11  
NUMBER OF SEQ ID NOS: 358  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 176  
; LENGTH: 5540  
; TYPE: DNA

ORGANISM: Homo sapiens  
US-09-918-715-176

## Alignment Scores:

Pred. No.: 8,21e-284 Length: 5540  
 Score: 3025.00 Matches: 564  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 13 Gaps: 0

US-09-970-076-6 (1-564) x US-09-918-715-176 (1-5540)

```

QY 1 MetAlatrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerIleuAlaThr 20
DB 144 ATGGCAGCGGAGGAGGAGGAGCCCTCGGCATCGGCTTCCAGTGGCTCTTTGGCCACT 203
QY 21 LeuValIleuIleCysAlaGlyGlnGlyValArgArgIleuArgGlyProAlaCysArg 40
DB 204 CTGGGTCTCATCTCGCGCGGCAAGGGAGCGACAGAGAGATGGGGGTCCAGCGCTGAC 263
QY 41 GlyGlyPheArgPheLeuTrpPheIleuArgIleuSerGlySerValIleuHisTrpAsn 60
DB 264 GCGGATTTGACCTGTACTCTCATTTTGGACAAATCAGAAAGTGTCTGCACACCTGAAAT 323
QY 61 GluIleTyTrpPheValGluGlnIleuAlaHisIleuPheIleSerProGlnIleuArgMet 80
DB 324 GAATCTATTACTTTGTGGAAACAGTTGGCTCCAAATTCATCAGCCCACTGAGAAATG 383
QY 81 SerPheIleValPheSerThrArgGlyThrThrIleuMetIleuThrGluAspArgGlu 100
DB 384 TCCCTTATTGTCTTCCACCGAGAAACAACTTAAATGAACTGACAGAAACAGAGAA 443
QY 101 GlnIleArgGlnIleuGluGlnIleuValIleuProGlnGlyAspThrThrMet 120
DB 444 CAATCCCTCAAGGCTGAGAAAGTCTGCAAGAAAGTCTGCAAGGAGAGACACTTACATG 503
QY 121 HisGluGlyPheGluArgAlaSerGlnGlnIleTyTrpGluAsnArgGlnIleTyArg 140
DB 504 CATGAGAGATTTGAAAGGCGCGAGTGAAGATTTTATGAAACAGCAAGGAGTACAG 563
QY 141 ThrAlaSerValIleIleAlaIleuThrArgGlyIleuHisGluAspPhePheTy 160
DB 564 ACAGCAGACGCTCATCTGCTTGAATGAGAACTCCATGAAAGATCTTTTTCAT 623
QY 161 SerGluArgGluAlaAsnArgSerArgArgIleuGlyAlaIleValIleCysValGlyVal 180
DB 624 TCAAGAGAGAGAGCTAATAGTCTCGAGATCTTGTGCATTTGTTACTGTGTGTG 683
QY 181 LysAspPheAsnGluThrGlnIleuAlaArgIleAlaAspSerIleuAspHisValPhePro 200
DB 684 AAAAGTTTCATGAGACACAGCTGCGCGGATGCGGACAGTAAAGATCATGTGTTC 743
QY 201 ValAsnArgGlyPheGlnAlaIleuGlnGlyIleIleHisSerIleuIleuLysSerCys 220
DB 744 GTGATGACGCGCTTCAAGCTCTGCAAGGACATCATCTCAATTTTGAAGAAGCTTC 803
QY 221 IleGluIleuAlaIleGluProSerThrIleCysAlaGlyIleuSerPheGlnValVal 240
DB 804 ATCGAATTTCTAGCAGCTGAAACCACTCCAAATGTGAGAGAGATCATTTCAAGTTTC 863
QY 241 ValArgGlyAsnGlyPheArgHisAlaIleArgAsnValAspArgValIleuCysSerPheLys 260
DB 864 GTGAGAGAGAAACGCTTCCGACATCCCGCAACGTCGACAGGCTCTTGCAGCTTCAAG 923
QY 261 IleAsnAspSerValThrIleuAsnGlnIleuProPheSerValGluAspThrTyIleuLeu 280
DB 924 ATCATATGACTCGGTCACTCATATGAGAAAGCCCTTTCTGTGGAAGATATCTTACTG 983
QY 281 CysProAlaProIleuIleuLysGluValGlyMetIleuAlaIleuGlnValSerMetAsn 300
DB 984 TGTCCAGGCGCTCATCTTAAAGAAAGTGGCAAGAAAGCTGCACTCCAGGTGACATGAA 1043
  
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QY 301 AspGlyLeuSerPheIleSerSerValIleIleThrThrHisCysSerAspGly 320
DB 1044 GATGGCTCTCTTTTATCTCAAGTTCTGTGATATGACCAACACACTGTGTCAGCGGT 1103
QY 321 SerIleIleuAlaIleAlaIleuIleuPheIleuIleuAlaIleuIleuTrp 340
DB 1104 TCCATCTCGGCAATCGGCTGCTGATCTGTCTCTGCTGCTGCTGCTGCTGCTGCTG 1163
QY 341 TrpPheTrpProLeuCysCysThrValIleIleIleGluValProProProAlaGlu 360
DB 1164 TGGTTCGCGCCCTCTCTCTGCACTGTATTTCAAGAGTCTCTCCACCCCTGCGGAG 1223
QY 361 GluSerGluGluIleuAspAspArgIleuProIleuLysIleuTrpProThrValAspAla 380
DB 1224 GAGAGTAGAGAAAGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1283
QY 381 SerTyTrpGlyGlyValGlyValGlyValIleuArgMetGluValArgTrpGlyGlu 400
DB 1284 TCTTATTATGTGGAGAGCGGTGGAGCATTTAAAGAAATGGAGTTCGTTGGGAGAA 1343
QY 401 LysGlySerThrGluGluGluValAlaIleuGluIleuValAlaIleuValIleuMet 420
DB 1344 AAGGCTCCACAGAAAGAGTGTCTGATTTGAAAGGCAAGAAATGCAAGTCAAGATG 1403
QY 421 ProGluGlnIleuTyTrpPheProGluProArgAsnIleuAsnAsnMetArgArgPro 440
DB 1404 CCGGAGCAGGAAATATGAAATCCCTGAGCCCGGAAATCTCAACAAATATGCGTCGGCT 1463
QY 441 SerSerProArgIleuTyTrpTySerProIleuLysGlyIleuIleuAlaIleuTrpValIleu 460
DB 1464 TCTTCCCGCGGAGGTGTCTCTCCAAATCAGGAAATCGATGCTGTGGGTCTTA 1523
QY 461 LeuArgLysGlyTyTrpAspArgValSerValMetArgProGlnProGlyAspThrGlyArg 480
DB 1524 CTGAGAAAGATATGATGCTGTGTCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTG 1583
QY 481 CysIleAsnPheThrArgValLysAsnAsnGlnProAlaIleTyTrpProLeuAsnAla 500
DB 1584 TGCATCAATCTTCAACAGAGGTCAAGAAACACAGCAGCAAGTATCCATCAACAGCC 1643
QY 501 TyHisThrSerSerProProProAlaProIleTyThrProProProProAlaProHis 520
DB 1644 TACCAACCTCTCTGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1703
QY 521 CysProProProProProSerAlaProThrProProIleProSerProProSerThrIleu 540
DB 1704 TGCCCTCCCGCGCCCGCCAGCGCCCTTACCCTCCATCCCGTCCCACTTCCACCTT 1763
QY 541 ProProProProGlnAlaProProProAsnArgAlaProProProSerArgProProPro 560
DB 1764 CCCCTCTCTCCGAGGCTCCACCTCCCAACAGGGCACTCTCTCTCCGCTCCGCTCCA 1823
QY 561 ArgProSerVal 564
DB 1824 AGGCTTCTGTTC 1835
  
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## RESULT 2

US-09-918-715-231

; Sequence 231, Application US/09918715

; Publication No. US20030017157A1

; GENERAL INFORMATION:

; APPLICANT: Brad St. Croix

; APPLICANT: Bert Vogelstein

; APPLICANT: Kenneth Kinzler

; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS

; FILE REFERENCE: 1107.00134

; CURRENT APPLICATION NUMBER: US/09/918, 715

; CURRENT FILING DATE: 2001-08-01

; PRIOR APPLICATION NUMBER: 60/222,599

; PRIOR FILING DATE: 2000-08-02

; PRIOR APPLICATION NUMBER: 60/224,360

; PRIOR FILING DATE: 2000-08-11

; PRIOR APPLICATION NUMBER: 60/282,850



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; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 231
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-715-231

Alignment Scores:
Pred. No.:      8,216-284      Length:      5540
Score:          3025.00        Matches:      564
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    100.00%       Indels:      0
DB:             13            Gaps:       0

US-09-970-076-6 (1-564) x US-09-918-715-231 (1-5540)

QY      1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerIleuAlaThr 20
DB      144 ATGGCCAGCGCGAGCGAGAGCCCTCGGCATGGCTTCACATGGCTCTTTGGCCACT 203
QY      21 LeuValIleuIleCyAlaGlyGlnGlyIleArgArgIleuAspGlyGlyProAlaCySer 40
DB      204 CTGGTCTCTATTCGGCCGGGCGGAGGGGAGCCAGGAGGATGGGGGTCCAGCCCTGATC 263
QY      41 GlyIlePheAspLeuIlePheIleuAspIleSerGlySerValIleuHisIleTrpAsn 60
DB      264 GCGCGATTTGACCTTACTTCACTTTTGACCAATCAGAAAGTGTCTGCACCATCGAAT 323
QY      61 GuileTyTyTyPheValGlnGlnIleuAlaHisIleuPheIleSerProGlnIleuAsn 80
DB      324 GAAATCTATTTACTTGTGGACAGTGGCTCAAAATTCATCAGCCCAAGTTGAGAAATG 383
QY      81 SerPheIleValPheSerThrArgGlyThrThrIleuMetIleuThrGluAspArgGlu 100
DB      384 TCTCTTATTTGTTTCTCCACCGGAGGAAACACTTATATGAACACAGAAAGACAGAGA 443
QY      101 GlnIleArgGlnGlyLeuGlnGlnIleuGlnIleuValIleuProGlyIleuAspThrTy 120
DB      444 CAAATCCGTCAGAGGCTAGAGAACTCCAGAAAGTTCTGCCAGGAGGACACTTATACG 503
QY      121 HisGlnGlyPheGluAspArgIleSerGlnIleTyTyTyGluAsnAspArgGlnIleTy 140
DB      504 CATGAGAGATTTGAAAGGCGCAGTAGCAGATTATATGAAACACAGAAAGGATACAGG 563
QY      141 ThrAlaSerValIleIleAlaLeuThrAspGlyIleuHisIleGluAspLeuPheTy 160
DB      564 ACGCCAGGCTCATCTCTTGTGACTGATGAGAACTCCATGAAGATCTCTTTTCTAT 623
QY      161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyTyCyAlaGlyVal 180
DB      624 TCAGAGAGGAGGCTATATGATGCTCGAGATCTTGCGCAATGTTACTGTTGGTGGG 683
QY      181 LysAspPheAsnGlnIleThrGlnIleuAlaArgIleAlaAspSerIleuAspHisIlePhe 200
DB      684 AAAGATTTCAATGACACACAGCTGGCGCGATGGCGACAGTAAAGATCATGTGTTCCC 743
QY      201 ValIleAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleuIleuValIleuSer 220
DB      744 GTGAATGACGCTTTCAGGCTCTGCAAGGATCATCTCACTCAATTTTGAAGAAGCTCC 803
QY      221 IleGlnIleLeuAlaAlaGluProSerThrIleCyAlaGlyIleuSerPheGlnVal 240
DB      804 ATCGAAATTTCTAGCAGCTGAACCATCCATATGTCAGAGAGATCATTTCAAGTTGTC 863
QY      241 ValIleArgIleAsnGlyPheArgHisIleAlaArgAsnValAspArgValIleuCySerPhe 260
DB      864 GTGAGAGGAAACGCTTCCGACATGCCCAACGTGACAGAGGCTCTTGCAGCTTCAAG 923
QY      261 IleAsnAspSerValThrIleuAsnGlnIleuProPheSerValGluAspThrTyTrpLeu 280

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DB      924 ATCAATGACGCTGACACTCAATGAGAAAGCCCTTTCTGTGAGATACTTATTACTG 983
QY      281 CysProAlaProIleLeuIleuValGlyMetIleValAlaLeuGlnValSerMetAsn 300
DB      984 TGTCCAGGCTTACTTAAAGAAAGTTGGCATGAAAGTGCATCTCCAGTACGATGAAAC 1043
QY      301 AspGlyLeuSerPheIleSerSerSerValIleIleThrTrpHisIleCysSerAspGly 320
DB      1044 GATGCGCTCTCTTTATCTCCAGTTCTGATCATCATCACACACACACTGTTGACCGT 1103
QY      321 SerIleLeuAlaIleAlaLeuIleuIleuPheLeuLeuAlaLeuAlaLeuTrp 340
DB      1104 TCCATCTCGGCGCATCGCCCTCTGATCTGTCTCTGCTCCAGCCCTGCTCTCTG 1163
QY      341 TrpPheTrpProLeuCysCysThrValIleIleIleValIleProProProAlaGlu 360
DB      1164 TGGTTCTGCCCCCTGCTGCACTGTGATTTATCAAGAGAGTCTCTCCACCCCTGCCAG 1223
QY      361 GluSerGlnGlnIleuAspAspAspGlyLeuProIleuIleuTrpProThrValAspAla 380
DB      1224 GAGAGTGAGAAAGAAAGATGATGCTGCTCAAGAAAGTGGCCAAACGATAGACCC 1283
QY      381 SerTyTyTyGlyIleArgGlyValGlyIleIleuArgMetGluValArgTrpGlyGlu 400
DB      1284 TCTTATTTATGGTGAGAGGCGTTGAGAGCATTAAGAAAGAGTTCTGTTGGAGAGAA 1343
QY      401 LysGlySerThrGlnGlnGlnIleuGlnIleuValIleuValIleuValIleuValIleu 420
DB      1344 AAGGCTCCACAGAAAGAGTGTCTAAGTTGAAAGGCAAGAAAGTCAAGATCAAGATG 1403
QY      421 ProGlnGlnGlnIleuPheProGlnIleuProArgAsnIleuAsnAsnMetArgArgPro 440
DB      1404 CCGAGCAGAGATATGATTCCTGAGCGCGGAATCTCAACACAAATATGCTGGCT 1463
QY      441 SerSerProArgIleTyTyTySerProIleuIleuGlyIleuAspAlaLeuTrpValIleu 460
DB      1464 TCTTCCCCCGGAGTGTACTCTCCATCAAGGAAATCTCGATGCTTGGGTCTCTA 1523
QY      461 LeuArgIleGlyTyTyTyAspArgValSerValMetArgProGlnProGlyIleuArg 480
DB      1524 CTGAGAAAGATATGATGCTGTGTGATGCTCCACAGCCAGGAGACAGGGGGGC 1583
QY      481 CysIleAsnPheThrArgValIleAsnAsnGlnProAlaIleTyTyTyProLeuAsnAla 500
DB      1584 TGCATCACTTCCACAGGCTCAAGAAACACAGCAGCAGCACTACCACTCAACAGCC 1643
QY      501 TyrHisIleSerSerProProProAlaProIleTyTyTyProProProProAlaProHis 520
DB      1644 TACCAACACTCTCGCCCTCTGCGCCCATCTCACTCCCTCCCTCTGCGCCGAC 1703
QY      521 CysProProProProProSerAlaProThrProIleProSerProProSerThrIleu 540
DB      1704 TGCCCTCCCGCCCGCCCGGCGCCCTTACCCCTCCATCCGTCCTCCACCTTCCACCT 1763
QY      541 ProProProProGlnAlaProProProAsnArgAlaProProProSerArgProProPro 560
DB      1764 CCCCTCTCTCCAGGCTCCACTCCCAACAGGACCTCTCTCTCCCGCTCTCTCA 1823
QY      561 ArgProSerVal 564
DB      1824 AGGCTTCTGTC 1835

RESULT 3
US-10-301-822-198
; Sequence 198, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kametkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.

```

APPLICANT: Thibodeau, Stephen N.  
APPLICANT: Burgart, Lawrence J.  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
TITLE OF INVENTION: THERAPY OF COLON CANCER  
FILE REFERENCE: MEM01-0292PRUN  
CURRENT APPLICATION NUMBER: US/10/301,822  
CURRENT FILING DATE: 2002-11-21  
PRIOR APPLICATION NUMBER: US 60/339,971  
PRIOR FILING DATE: 2001-12-10  
PRIOR APPLICATION NUMBER: US 60/361,978  
PRIOR FILING DATE: 2002-03-05  
PRIOR APPLICATION NUMBER: US 60/381,988  
PRIOR FILING DATE: 2002-05-20  
NUMBER OF SEQ ID NOS: 228  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 198  
LENGTH: 5540  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (144)...(1838)  
US-10-301-822-198  
Alignment Scores:  
Pred. No.: 8,21e-284 Length: 5540  
Score: 3025.00 Matches: 564  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 15 Gaps: 0  
US-09-970-076-6 (1-564) x US-10-301-822-198 (1-5540)  
OY 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20  
Db 144 ATGGCCACGGCGAGCGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTTTGGCCACT 203  
OY 21 LeuValLeuIleCysAlaGlyGlnGlyArgArgGluAspGlyGlyProAlaCysPyr 40  
Db 204 CTGGGCTCATCTGGCCGGGACAGGGAGCCAGAGAGATGGGGGTCCAGCCCTGCTAC 263  
OY 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60  
Db 264 GCGCGATTGACCTGACTCTTCTTGGCAAAATCAGAAAGTCTCTGACACCTGGAAT 323  
OY 61 GluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80  
Db 324 GAATCTATTACTTGTGGACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGATG 383  
OY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100  
Db 384 TCTTTATTGTTTCTCCACCGAGAGAACATTAATGAAATGACAGAAAGACAGAA 443  
OY 101 GlnIleArgGlnGlyLeuGluGlnLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120  
Db 444 CAATCCGTCAGAGCGCTTGAAGAACTCCAGAAAGTCTGCGCAGAGAGACACTTACATG 503  
OY 121 HisGluGlyPheGluArgAlaSerGlnGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140  
Db 504 CATGAGAGATTGAAAGGGCCAGTACAGCAGATTTATTGAAACAGACAGAGGTTACAG 563  
OY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluMetHisGluAspLeuPhePheTyr 160  
Db 564 ACAGCCAGGCTATCATTTGCTTGTGACTGATGAGAACTCCAGAAAGATCTTTTCTAT 623  
OY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValIleTyrCysValGlyVal 180  
Db 624 TCAGAGAGAGAGGCTTAATAGCTCTGAGATCTTGGTGCATTTTACTGTGTGTG 683  
OY 181 LysAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200

Db 684 AAAGATTTCATGAGACAGCTGGCCCGGATTGCGGACAGTAAGATCATGTGTTCCC 743  
OY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220  
Db 744 GTGAATACGGCTTTCAGGCTCTGCAAGCATCATTCACCTCAATTTGAAAGATCTTGC 803  
OY 221 IleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGlySerPheGlnVal 240  
Db 804 ATCAAAATTCATGAGAGCTGAACCATTCACCATATGTCAGAGAGAGTCAATTCAGTTGTC 863  
OY 241 ValArgGlyAsnGlyPheAlaGlnAlaArgAsnValAspArgValLeuCysSerPheLys 260  
Db 864 GTGAGAGAAACCGCTTCCAGCATGCCCCGAGACGTGACGGGTCTCTCCACCTTCAG 923  
OY 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspTrpTyrLeuLeu 280  
Db 924 ATCAATGACTCGGTCACTCATAGAGAGCCCTTTCTGTGAAAGTACTTATTTACTG 983  
OY 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300  
Db 984 TGTCAGCGCCTATCTTAAAGAAAGTTGGCATGAAAGCTGCACCTCCAGTCAGCATGAC 1043  
OY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrThrIleCysSerAspGly 320  
Db 1044 GATGGCTCTCTTTTATCTCCAGTTCTGTCAATCATCAACACACACTGTTCTGACGGT 1103  
OY 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuTrp 340  
Db 1104 TCCATCTGGGCATCGCCCTGTGATCTCTGCTCTGCTTCAAGCCCTGCGCTCTCTGG 1163  
OY 341 TrpPheTrpProLeuCysCysTrpValIleIleLysGluValProProProAlaGlu 360  
Db 1164 TGGTTTGGCCCTCTGCTGACGTGATTATCAAGAGAGGCTCCACCCCTGCGCAG 1223  
OY 361 GluSerGluGluGluAspAspAspGlyLeuProLysLysLysTrpProThrValAspAla 380  
Db 1224 GAGAGTAGAGAAAGATGATGATGCTGCTCAAGAAAGAGTGGCCACAGTGAAGGCC 1283  
OY 381 SerTyrTyrGlyGlyArgGlyValGlyIleLysAspMetGluValArgTrpGlyGlu 400  
Db 1284 TCTTATTATGGTGGAGAGGCGTTGGAGCATTAAGAAATGAGAGTTCGTTGGGAGAA 1343  
OY 401 LysGlySerThrGluGlnGlyAlaLysLeuGlnLysAlaLysAsnAlaArgValLysMet 420  
Db 1344 AAGGCTCCACAGAAAGAGGTGCTAAGTTGAAAGCAAGATGCAAGGTCAAGATG 1403  
OY 421 ProGluGlnGlyTyrGluPheProGluProArgAsnLeuAsnAsnMetArgArgPro 440  
Db 1404 CCGAGAGAGAAATATGAATTCCTGAGCCCGCAATCTCAACAATATGCGCTGCGCT 1463  
OY 441 SerSerProArgLysTrpTyrSerProIleLysGlyLysLeuAspAlaLeuTrpValLeu 460  
Db 1464 TCTTCCCCCGAAGGTACTCTCCAAATCAAGGAAATCTCGATGCTGTGGGTCTTA 1523  
OY 461 LeuArgLysGlyTyrAspArgValSerValMetArgProGlnProGlyAspThrGlyArg 480  
Db 1524 CTGAGAAAGATATGATCGGTGTCTGTGATGCTGCACAGCAGAGACACGGGGGCG 1583  
OY 481 CysIleAsnPheThrArgValLysAsnAsnGlnProAlaLysTyrProLeuAsnAsnAla 500  
Db 1584 TGCAATCAACTTCACAGAGGTCAAGAACACAGCAGCCCAAGTACCACTCAACAAAGGCC 1643  
OY 501 TyrHisThrSerSerProProProAlaProIleTyrThrTrpProProProProAlaProHis 520  
Db 1644 TACCACACTCTCTGCGGCTCTGCCCCCACTTCACTCCCACTCTCTGCGCCCCAC 1703  
OY 521 CysProProProProProSerAlaProThrProProIleProSerProProSerThrLeu 540  
Db 1704 TGCCCTCCCCCGCCCGCCAGCGCCCTTACCCCTCCATCCGCTCCACCTTCACCTT 1763  
OY 541 ProProProProGlnAlaProProProAsnArgAlaProProProSerArgProProPro 560  
Db 1764 CCCCCTCTCCCGCGCTCCACCTCCCAAGGGCAGCTCTCTCTCCGCGCTCTTCCA 1823





OY 529 rothrhp:rofi:leproser:ProProserThleu:ProProProGlnAla:ProPro 548  
 DB 1852 CCACCTCTCCCATCTCTTCCCCACCATCATCTCTCCCCCTCTCTCCAGGCCCCACCC 1911  
 OY 549 ProAnaGAla:ProProProSerArgProProProArgProSerVal 564  
 DB 1912 CCTAACAGAGGACCTCCCCCTCCGACCTCCTCAAGGCTTCTGTC 1959  
 RESULT 6  
 US-10-302-172-250  
 / Sequence 250, Application US/10302172  
 / Publication No.: US20040053250A1  
 GENERAL INFORMATION:  
 APPLICANT: Tang, Y. Tom  
 APPLICANT: Xue, Aidong J.  
 APPLICANT: Dimaec, Radoje T.  
 TITLE OF INVENTION: No. US20040053250A1 Arginine-rich Protein-like Nucleic Acids ar  
 TITLE OF INVENTION: Polypeptides  
 FILE REFERENCE: 803 ICNCP  
 CURRENT APPLICATION NUMBER: US/10/302,172  
 CURRENT FILING DATE: 2002-11-21  
 PRIOR APPLICATION NUMBER: US 10/225,251  
 PRIOR FILING DATE: 2002-08-20  
 PRIOR APPLICATION NUMBER: PCT US02/05095  
 PRIOR FILING DATE: 2002-03-05  
 PRIOR APPLICATION NUMBER: US 09/799,451  
 PRIOR FILING DATE: 2001-03-05  
 NUMBER OF SEQ ID NOS: 950  
 SOFTWARE: PC\_FGenes Version 2.0  
 SEQ ID NO 250  
 LENGTH: 3981  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (297)..(1118)  
 US-10-302-172-250  
 Alignment Scores:  
 Pred. No.: 2.5e-186 Length: 3981  
 Score: 2022.00 Matches: 372  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatch: 0  
 Query Match: 66.84% Indels: 0  
 DB: Gaps: 0  
 US-09-970-076-6 (1-564) x US-10-302-172-250 (1-3981)  
 OY 193 AepserLrVaBpRhLeValPheProValAmdnBpGlyPheGlnAlaLeuGlnGlyIle 212  
 DB 3 GACAGTAAAGGATCATGTGTTCCCGTGAATGACCGCTTCAGGCTTCGCAAGGATCATC 62  
 OY 213 HtserLleuLrValYLeSerCysIleGluIleuAlaIleGluProSerThrIleCys 232  
 DB 63 CACTCAATTTGAGAGAAAGTCTCTGCATCGAAATTCAGAGAGCTGAACATCAACATATGT 122  
 OY 233 AlAglyGlnSerPheGlnValValValArgGlyAengIyPheArgHleAlaArgAnVal 252  
 DB 123 GCAGAGAGATCATTTCAAGTTGCTCGTAGAGAGAAACGGCTTCGACATGCCGCAACGTG 182  
 OY 253 AepAqVAlleuCysSerPheLysIleAmdnBpSerValThrIleAengIlyPhePro 272  
 DB 183 GACAGGATCTCTGACGCTTCAGATCAATGACTGAGTCACTCAATGATGAGAGCCCTTT 242  
 OY 273 SerValGlnAspThrTyrLeuLeuCysProAlaProIleLeuLysGluValGlyMetLys 292  
 DB 243 TCTGGAGAAATATTATTACTGTGTCAAGGCTTATCTTAAAGAGAGTTGGCATGAA 302  
 OY 293 AlaAlaLeuGlnValSerMetAsnBpGlyLeuSerPheIleSerSerValIleIle 312  
 DB 303 GCTGACATCCAGGTAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 362

[illegible]

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/ PRIOR FILING DATE: 1999-03-01
/ PRIOR APPLICATION NUMBER: 09/312,359
/ PRIOR FILING DATE: 1999-05-14
/ PRIOR APPLICATION NUMBER: 09/336,536
/ PRIOR FILING DATE: 1999-06-18
/ PRIOR APPLICATION NUMBER: 09/342,687
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: 09/345,464
/ PRIOR FILING DATE: 1999-06-30
/ PRIOR APPLICATION NUMBER: 09/365,164
/ PRIOR FILING DATE: 1999-07-30
/ PRIOR APPLICATION NUMBER: 09/399,723
/ PRIOR FILING DATE: 1999-09-20
/ PRIOR APPLICATION NUMBER: 09/409,634
/ PRIOR FILING DATE: 1999-09-30
/ PRIOR APPLICATION NUMBER: 09/471,179
/ PRIOR FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: 09/474,071
/ PRIOR FILING DATE: 1999-12-29
/ PRIOR APPLICATION NUMBER: 09/474,072
/ PRIOR FILING DATE: 1999-12-29
/ PRIOR APPLICATION NUMBER: 09/514,010
/ PRIOR FILING DATE: 2000-02-25
/ PRIOR APPLICATION NUMBER: 09/516,745
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: 09/572,002
/ PRIOR FILING DATE: 2000-05-14
/ PRIOR APPLICATION NUMBER: 09/597,993
/ PRIOR FILING DATE: 2000-06-19
/ PRIOR APPLICATION NUMBER: 09/599,596
/ PRIOR FILING DATE: 2000-06-22
/ PRIOR APPLICATION NUMBER: 09/630,334
/ PRIOR FILING DATE: 2000-07-31
/ PRIOR APPLICATION NUMBER: 09/606,565
/ PRIOR FILING DATE: 2000-06-29
/ PRIOR APPLICATION NUMBER: 09/606,317
/ PRIOR FILING DATE: 2000-06-29
/ PRIOR APPLICATION NUMBER: 09/665,666
/ PRIOR FILING DATE: 2000-09-20
/ PRIOR APPLICATION NUMBER: 09/677,751
/ PRIOR FILING DATE: 2000-09-30
/ NUMBER OF SEQ ID NOS: 162
/ SEQ ID NO 23
/ LENGTH: 4417
/ TYPE: DNA
/ ORGANISM: Mouse
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (3)...(1145)
/ US-09-796-753-23

Alignment Scores:
Pred. No.: 8,886-186 Length: 4417
Score: 2017.00 Matches: 371
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 98.15% Mismatches: 4
Query Match: 66.68% Indels: 0
DB: 10 Gaps: 0

US-09-970-076-6 (1-564) x US-09-796-753-23 (1-4417)

Qy 187 GlnleuAlaArgIleAlaAspSerLyAspHisValPheProValAsnAspGlyPheGln 206
Db 12 CAGTTGGCTCGGATTGCAGACAGTAAGACACGCTTTCCTGTAAGACGCGCTTCCAG 71
Qy 207 AlaLeuGlnGlyIleIleHisSerIleLeuLylySerCysIleGluIleuAla 226
Db 72 GCTCTCCAGGCGATTATCCATCAATTTAAAGAAATCCTGCATCGAAATTCGCGCGCT 131
Qy 227 GluProSerThrIleCysAlaGlyGlySerPheGlnValValArgGlyAsnGlyPhe 246
Db 132 GAACATTCACCATCTGCGCGGAGAGTCTTTCAAAGTGCTGTAAGAGAAATGCGCTTC 191
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Qy 247 ArgHisAlaArgAsnValAspArgValLeuCysSerPheLyIleAsnAspSerValThr 266
Db 192 CGACATGCCCGCATGTGACAGGGCTCCTGACAGTTCAAAATCAATGACTCAGTACAG 251
Qy 267 LeuAsnGlyLysProPheSerValGluAspThrTyrtleuLeuCysProAlaProIleu 286
Db 252 CTCAATAGAAAGCCCTTGTGCGAAGACACTTAATTTGCTGTGCCAGCACCAATCTTG 311
Qy 287 LysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsnAspGlyLeuSerPheIle 306
Db 312 AAAGAAGTTGGATGAAGAGCTGCAGCTCAGTCAGATGAAGACAGGCTCTCTTCA 371
Qy 307 SerSerSerValIleIleThrThrHisCysSerAspGlySerIleLeuAlaIleAla 326
Db 372 TCAGTTCTGTCAATCATCACCAACACACTGTTCAAGCGGCTCCATCTCGCATGCT 431
Qy 327 LeuLeuIleuPheLeuLeuAlaLeuAlaLeuLeuTrpTrpPheTrpProLeuCys 346
Db 432 CTGCTGTCTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 491
Qy 347 CysThrValIleIleLysGluValProProProProAlaGluGluSerGluGluAsp 366
Db 492 TGCAAGATGATCATCAAGAGAGTCCCTCCACCCCTCTTGAAGAGAGTGAAGAAAGC 551
Qy 367 AspAspGlyLeuProLysLysLysTrpProThrValAspAlaSerTyrtGlyGlyArg 386
Db 552 GATGATGTTTGCAGAAAGAAATGAGCCCACTAGATGCTCTTATGAGTGAAGC 611
Qy 387 GlyValGlyGlyIleLysArgMetGluValArgTrpGlyGlyLysSerThrGluGlu 406
Db 612 GGTGTGGAGGCAATTAAGAGATGAGGTCCGTGGGAGAAAGGCTCCACAGAAAGAA 671
Qy 407 GlyAlaLysLeuGluLysAlaLysAlaArgValLysMetProGluGlnGlyTyrtGlu 426
Db 672 GGGCGCAAGTTAGAAAGGCAAGAAATGACAGATCAAGATCCAGAGCAAGAAATAG 731
Qy 427 PheProGluProArgAsnLeuAsnAsnMetArgArgProSerSerProArgLysTrp 446
Db 732 TTCCCAAGAAACCCGAAACCTCAACAAACATGCGCGGCTCTCTGCGCTCGAAGTGG 791
Qy 447 TyrtSerProIleLysGlyLysLysAspAlaLeuTrpValLeuLeuAlaGlyLysGly 466
Db 792 TACTGCCCAACAAAGGAGAACTGATGCTGTGTGCTGTGAGAAAGATATGAC 851
Qy 467 ArgValSerValMetCysProGluInProGlyAspThrGlyArgCysIleAsnPheThrArg 486
Db 852 CGAGTCTGTGATGAGAGCCACAGCAGAGACAGGAGCCCTGTATCAATTCAACAGA 911
Qy 487 ValLysAsnAsnGlnProAlaLysTyrtProLeuAsnAsnAlaTyrtHisSerSerPro 506
Db 912 GTGAAGAAACAGTACGACAGCCAAAGTATCCCTGAACAAACCTACACCCAGCTCCCA 971
Qy 507 ProProAlaProIleTyrtThrProProProProAlaProHisCysProProProPro 526
Db 972 CTTCCCGCTCTATCTACACACCCCAACCCCTCTCCCACTCCCTCCCAAGCCCCC 1031
Qy 527 SerAlaProThrProProIleProSerProProSerThrLeuProProProGluAla 546
Db 1032 AGTCCCCCACTCTCTCCATCTCTCCCAACATCACTCTCCCTCCCTCTCTCAGGCC 1091
Qy 547 ProProProAsnAlaAlaProProProProSerArgProProProArgProSerVal 564
Db 1092 CCACCCCTTAACAGGAGCACTCCCTCCGACCTCTCCAAAGGCTTGTGTC 1145

RESULT 8
US-10-038-307-3
; Sequence 3, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
```

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; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FASTSEQ for Windows, Version 4.0
; SEQ ID NO 3
; LENGTH: 4417
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(1145)
US-10-038-307-3

Alignment Scores:
Pred. No.: 8,886-186 Length: 4417
Score: 2017.00 Matches: 371
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 98.15% Mismatches: 4
Query Match: 66.68% Indels: 0
DB: 15 Gaps: 0

US-09-970-076-6 (1-564) x US-10-038-307-3 (1-4417)
Qy 187 GlnleuAlaArgIleAlaAspSerIysAspHisValPheProValAsnAspGlyPheGln 206
Db 12 CAGTGGCTCGGATTGACAGACAGTAAGACACGAGTTCCTGTAACACACGCGCTTCCAG 71
Qy 207 AlaLeuGlnGlyIleIleHisSerIleLeuIleuIleuIleuIleuIleuIleuIleuIleu 226
Db 72 GCTCTCCAAAGGCAATTCACATCAATTTAAAGAAATCTGATGAAATTTGGCGGCT 131
Qy 227 GluProSerThrIleCysAlaGlySerPheGlnValValArgGlyAsnGlyPhe 246
Db 132 GAACCATCCACCATCTGCGCGGAGAGTCTTCAAGTGTGTAAAGAGAAATGCGCTTC 191
Qy 247 ArgHisAlaArgAsnValAspArgValIleuCysSerPheIleIleAsnAspSerValThr 266
Db 192 GCACATGCCCCGAAAGTGACAGGGCTCTCAGCTTCAAAATCAATGACTCAGTCACG 251
Qy 267 LeuAsnGlyIleProPheSerValGluAspThrIleuIleuIleuIleuIleuIleuIleu 286
Db 252 CTCATATGAAAGCCCTTCTGCTGAGAAACATTTATTTGCTGCTGCGACCAATCTTG 311
Qy 287 IysGluValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 306
Db 312 AAAGAAGTTGGCATGAAGCTGACAGTCAGATGACGACGAGCGCTGCTTCATC 371
Qy 307 SerSerSerValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 326
Db 372 TCACATTCGTGATCATATCACACACACACTGTCAGAGGCTCCATCTGCGAGATTCCT 431
Qy 327 LeuLeuIleLeuPheIleuLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 346
Db 432 CTGCTGCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 491
Qy 347 CysThrValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 366
Db 492 TCACAGTATCATCATCAAGAGAGTCCCTCACCCCTGTTGAGAGAGTGAAGAGAGAGAGAG 551
Qy 367 AsnAspGlyLeuProIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 386
Db 552 GATGATGATTTTCCAAAGAAAGAAATGGCCACAGATGATGCTCTTATATATGATGAGCC 611
Qy 387 GlyValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 406
Db 612 GGTGCGGAGGCAATTAAGAAATGAGAGTCCGCTGGGAGAAAGGCTCCACAGAGAA 671
Qy 407 GlyAlaIleuGluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIle 426
Db 672 GGGGCGAAGTTAGAAAGCAAGAAATGACAGGATCAAGATGCTCAGAGCAAGAAATATGAG 731
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Qy 427 PheProGluProArgAsnIleuAsnAsnMetArgArgProSerSerProArgIleIleIle 446
Db 732 TTCCAGAAACCCGAAACCTCAACAAACAAATGGCGGCTTCTGCTGCGAAATGG 791
Qy 447 TyrSerProIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 466
Db 792 TACTCGCCCATCAAGGAGAACTCGATCCCTGTGGTTCCTGCGAGAAAGATATGAC 851
Qy 467 ArgValSerValMetArgProGlnProGlyAspThrGlyArgCysIleAsnPheThrArg 486
Db 852 CGAGTGTGTGATGAGGCGACAGCAGAGACACGAGACCTGTATCACTTCACTCA 911
Qy 487 ValIysAsnAsnGlnProAlaIleIleIleIleIleIleIleIleIleIleIleIleIleIle 506
Db 912 GTGAAGAACACTGACCGGACCAAGATCCCTGAACAAACACTTACACCCAGCTCCCA 971
Qy 507 ProProAlaProIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 526
Db 972 CCTCCGCTCTCTATCTACACACCCCAACCCCTGCTCCCACTGCTCCCAAGCC 1031
Qy 527 SerIleProThrProProIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 546
Db 1032 AGTGCCCTCCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1091
Qy 547 ProProProAsnArgAlaProProProSerArgProProArgProSerVal 564
Db 1092 CACCCCTTAACAGGACCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1145

RESULT 9
US-10-201-292-3
; Sequence 3, Application 44/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4417
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(1145)
US-10-201-292-3

Alignment Scores:
Pred. No.: 8,886-186 Length: 4417
Score: 2017.00 Matches: 371
Percent Similarity: 98.94% Conservative: 3
Best Local Similarity: 98.15% Mismatches: 4
Query Match: 66.68% Indels: 0
DB: 15 Gaps: 0

US-09-970-076-6 (1-564) x US-10-201-292-3 (1-4417)
Qy 187 GlnleuAlaArgIleAlaAspSerIysAspHisValPheProValAsnAspGlyPheGln 206
Db 12 CAGTGGCTCGGATTGACAGACAGTAAGACACGAGTTCCTGTAACACACGCGCTTCCAG 71
Qy 207 AlaLeuGlnGlyIleIleHisSerIleLeuIleuIleuIleuIleuIleuIleuIleuIleu 226
Db 72 GCTCTCCAAAGGCAATTCACATCAATTTAAAGAAATCTGATGAAATTTGGCGGCT 131
Qy 227 GluProSerThrIleCysAlaGlySerPheGlnValValArgGlyAsnGlyPhe 246
Db 132 GAACCATCCACCATCTGCGCGGAGAGTCTTCAAGTGTGTAAAGAGAAATGCGCTTC 191
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247 ArgHisAlaArgAsnValAspArgValLeuCySerPheValLeuAsnAspSerValThr 266  
Db CGACATGCCCGCAATGTGACAGGGCTCCTGCGACCTTCAAAATCAATGACTGACG 251  
267 LeuAsnGluValProPheSerValGluAspThrTyrLeuLeuCyProAlaProIleLeu 286  
Db CTCATGTGAAGCCCTTGCTGTGAGACACTTATTGCTGTGCCAGCAATCTTG 311  
287 LysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsnAspGluLeuSerPheIle 306  
Db AAAGAGTTGGCATTAAGCTGCACTGCAAGTCAAGCAAGAGGCGCTTCTTCAATC 371  
307 SerSerSerValIleIleThrThrHisCySerAspGlySerIleLeuAlaIleAla 326  
Db TCCAGTTCTGTCATCATCACCCACACACTGTTCAAGCGGCTCATCTGGCATTCCT 431  
327 LeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTyrTyrPheTyrProLeuCy 346  
Db CTGCTGCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 491  
347 CysThrValIleIleIleValGluValProProProProAlaGluGluSerGluGluAsp 366  
Db TGCACAGTATCATCAAGAGGTCCCTCACCCCTGTTGAGAGAGTGAAGAGAGAGAC 551  
367 AspAspGlyLeuProLysLysLysLysLysLysLysLysLysLysLysLysLysLys 386  
Db GATGATGCTTTGCCAAGAAAGAAAGGCGCCACAGTAAAGTCTTATTATGATGAGCG 611  
387 GlyValGlyGlyIleLysArgMetGluValArgTyrGlyGlyLysSerThrGluGlu 406  
Db GCTGTGGAGGCGATTAAAGAAATGAGAGTCCGCTGGAGAAAGGCGCTCCACAGAA 671  
407 GlyAlaLysLeuGluValAlaLysAsnAlaArgValLysMetProGluGluTyrGlu 426  
Db GGGGGAAGTAAAGAAAGCAAGATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 731  
427 PheProGluProArgAsnLeuAsnAsnAsnMetArgArgProSerSerProArgLysTyr 446  
Db TTCCAGAAACCCCGAAACCTCAACAAACATGCGCGCGCTCTCTGCGTCCGAAAGTG 791  
447 TyrSerProIleLysGlyLysLeuAsnAlaLeuTyrValLeuLeuArgLysTyrAsp 466  
Db TACTCGCCCATCAAGGAAACTCGATGCTGTGTGCTGTGCTGTGCTGTGCTGTGCT 851  
467 ArgValSerValMetArgProGlnProGlnArgThrGlyArgCysIleAsnPheThrArg 486  
Db CGAGTGTCTGTATGAGGCACAGCCAGAGACAGGAGACGCTGTATCACTTCAACAGA 911  
487 ValLysAsnAsnGlnProAlaLysTyrProLeuAsnAsnAlaTyrHisThrSerSerPro 506  
Db GTGAAGAAACAGTCAAGCCAGCCAAAGTATCCCTGAAACAAACACTTACACCCAGCT 971  
507 ProProAlaProIleTyrThrProProProProAlaProHisCysProProProPro 526  
Db CCTCCGCTCTCATCTACACACCCCAACCCCTGCTGCCACTGCGCTCCCAAGCCCCC 1031  
527 SerAlaProThrProProIleProSerProProSerThrLeuProProProProGlnAla 546  
Db AGTGCCCCACATCCCTCCATTCCTTCCACACATCACTCCCTCCCTCCCTCAAGGCC 1091  
547 ProProProAsnArgAlaProProProSerArgProProProArgProSerVal 564  
Db CCAACCCCTTAACAGGCACTCCCTCCCTCCCACTCTCCCAAGGCTTCTGTC 1145

RESULT 10  
US-10-133-937-58

; Sequence 58, Application US/10133937

; Publication No. US20030207278A1

; GENERAL INFORMATION:

; APPLICANT: Khan, Javed

; APPLICANT: Ringner, Markus

; APPLICANT: Peterson, Carsten

; APPLICANT: Meltzer, Paul  
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,  
; DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND  
; TITLE OF INVENTION: OTHER BIOLOGICAL STATES  
; FILE REFERENCE: 11613.56US01  
; CURRENT APPLICATION NUMBER: US/10/133.937  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 58  
; LENGTH: 1454  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-133-937-58

Alignment Scores:

Score: 1.78e-174 Length: 1454  
Percent Similarity: 1894.00 Matches: 364  
Best Local Similarity: 100.00% Conservative: 0  
Query Match: 62.61% Mismatches: 0  
DB: 16 Gaps: 0

US-09-970-076-6 (1-564) x US-10-133-937-58 (1-1454)

1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTyrPheLeuSerLeuAlaThr 20  
Db ATGGCCACGGCGAGCGGAGAGGCGCTCGCATCGCTTCCAGTGGCTCTTGGCCACT 203  
21 LeuValLeuIleCysAlaGlyGlyGlyValArgArgGluAspGlyIleProAlaCysTyr 40  
Db CTGTGCTCATCTGCGCGCGGCAAGGGGAGCGAGGAGATGGGGCTCCAGCTGCTAC 263  
41 GlyIlePheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTyrAsn 60  
Db GCGGATTTGACCTGATCTTCAATTTGGAACAATCAGAAAGTGTGTCACACTGGAAT 323  
61 GluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80  
Db GAATTCATTACTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCACAGTTGAGATG 383  
81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100  
Db TCCCTTATTGTTTCTCCACCGGAGAAACCTTAATGAACATGACAGAAACAGAGAA 443  
101 GlnIleArgGlnGlyLeuGluGlnLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120  
Db CAAATCCGTCAAGGCTTGAAGAACTTCAGAAAGTTCTGCGAGAGAGACACTTACATG 503  
121 HisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140  
Db CATTAAGATTGTAAGAGGCGCAGTGAACAGATTATTAATGAACACAGAGGTTACAG 563  
504 CATTAAGATTGTAAGAGGCGCAGTGAACAGATTATTAATGAACACAGAGGTTACAG 563  
141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPheTyr 160  
Db ACAAGCCAGCTCATCATTTGCTTGAATGATGAGAACTCCATGAAGATCTTTTCTAT 623  
161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180  
Db TCAGAGGAGGAGGTAAATGAGTCTCGAGATCTTGATGCAATGTGTTACTGTGTGGTGG 683  
624 TCAGAGGAGGAGGTAAATGAGTCTCGAGATCTTGATGCAATGTGTTACTGTGTGGTGG 683  
181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200  
Db AAAGATTTCATTAAGACACAGCTGGCCCGAATTCGCGACAGTAAGATCATGTGTTCCC 743  
201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleHisSerIleLeuLysSerCys 220  
Db GTGAATGACGCTTTCAGGCTCTGCAAGGATCATTCACATTTTGAAGAAGTCTGCG 803  
744 GTGAATGACGCTTTCAGGCTCTGCAAGGATCATTCACATTTTGAAGAAGTCTGCG 803  
221 IleGluIleLeuAlaAlaGluProSerThrIleCysValAlaGlyLysSerPheGlnVal 240  
Db ATGAAATTCATGACGCTGAACCATTCACATATGTGACAGAGAGTCAATTCAGTGTGC 863



QY 241 ValArgGlyAenGlyPheArgHisAlaArgAenValAspArgValLeuCySerPheLeu 260  
 DB 864 GTGAGAGGAAACGGCTTCCGACATGCCCCGCAACGTGACAGGGTCTCTCGACGCTTCAAG 923  
 QY 261 ILeaAenAspSerValThrLeuAenGlyLysProPheSerValGluAspThrTyrLeuLeu 280  
 DB 924 ATCAATGACTCGGTCACTCACTCAATGAGAAAGCCCTTTCTGTGAGAGACACTTATTACTG 983  
 QY 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAen 300  
 DB 984 TGTCCAGCGCCCTATCTTAAAGAGTTGGCATGAAGCTGCACCTCAGTCAGCATGAAAC 1043  
 QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrThiCysSerAspGly 320  
 DB 1044 GATGCGCTCTCTTTATCTCCAGTTCTGTCATCATCACCAACACACACTGTTCTGACGGT 1103  
 QY 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTrp 340  
 DB 1104 TCCATCTCGGCGCATGCGCCCTGCTGATCCTGTTCTGCTCCTAGCCCTGGCTCTCTGCG 1163  
 QY 341 TrpPheTrpProLeuCyCysThrValIleIleLysGluValProProProAlaGlu 360  
 DB 1164 TGGTTCTGGCCCTCTGCTGCACTGTGATTATCAAGAGGTCCCTCCACCCCTGCGAG 1223  
 QY 361 GluSerGluGlu 364  
 DB 1224 GAGAGTGAGGAA 1235

RESULT 11  
 US-10-159-563-58  
 ; Sequence 58, Application US/10159563  
 ; Publication No. US20040009154A1

GENERAL INFORMATION:  
 ; APPLICANT: Khan, Javed  
 ; APPLICANT: Ringner, Markus  
 ; APPLICANT: Peterson, Carsten  
 ; APPLICANT: Meltzer, Paul  
 ; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
 ; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS  
 ; FILE REFERENCE: 11613.56US11  
 ; CURRENT APPLICATION NUMBER: US/10/159,563  
 ; CURRENT FILING DATE: 2002-12-09  
 ; PRIOR APPLICATION NUMBER: US 10/133,937  
 ; PRIOR FILING DATE: 2002-04-25  
 ; NUMBER OF SEQ ID NOS: 444  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 58  
 ; LENGTH: 1454  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-159-563-58

Alignment Scores:  
 Pred. No.: 1,78e-174 Length: 1454  
 Score: 1894.00 Matches: 364  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 62.61% Indels: 0  
 DB: 16 Gaps: 0

US-09-970-076-6 (1-564) x US-10-159-563-58 (1-1454)

QY 1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20  
 DB 144 ATGGCCACCGCGAGCGAGAGAGCCCTCGCATCGGCTTCAGTGGCTCTCTTGGCCACT 203  
 QY 21 LeuValLeuIleCysValGlyGlnGlyArgArgGluAspGlyGlyProAlaCysTyr 40  
 DB 204 CTGGGTCTATCTGGCCCGGCAAGGGGAGCGAGGAGAGTGGGGGTCCAGCCTGCTAC 263  
 QY 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAen 60  
 DB 264 GCGGAGTTTGACTGTACTTATTTTGGACAAATCAAGAAAGTGTGTGACCACTGGAAAT 323

QY 61 GluIleTyrTyrPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80  
 DB 324 GAATCTATTACTTTGTGGAAACAGTTGGCTACAAATTCATCAGCCCACTTGAGATG 383  
 QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100  
 DB 384 TCTTTATTGTTTCTCCACCGAGAAACAACCTTAATGAACATGACAGAAAGACAGAA 443  
 QY 101 GlnIleArgGlnGlyLeuGluGluLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120  
 DB 444 CAATCCGTCAAGCCTTAGAAGAACTCCAGAAAGTTCGACAGAGAGACACTTACATG 503  
 QY 121 HisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAenArgGlnGlyTyrArg 140  
 DB 504 CATGAAGATTGAAAGGCGCAGTGAAGATTTTATTTGAAACAGCAAGGGTACAGG 563  
 QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyr 160  
 DB 564 ACAGCCAGCGTCATCATTTGCTTGTGACTGATGAGAACTCCATGAAGATCTCTTTTCTAT 623  
 QY 161 SerGluArgGluAlaAsnArgSerThrArgAspLeuGlyAlaIleValTyrCysValGlyVal 180  
 DB 624 TCAGAGAGGAGGCTTAATAGGCTTCGAGATCTGTGTCAATTGTTACTGTGTGTGTG 683  
 QY 181 LysAspPheAenGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200  
 DB 684 AAAGATTTCATATGACACACAGCTGGCCGGAATGGGACATGAAGATCATGTGTTTCC 743  
 QY 201 ValAenAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220  
 DB 744 GTGAATGACGGCTTTCAGGCTCTGCAAGGCAATCATCCACTCAATTTTGAAGAGTCCGC 803  
 QY 221 IleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240  
 DB 804 ATCGAAATTCAGAGCTGAACCACTCCATATGTGACAGAGAGTCAATTCAGATTGTC 863  
 QY 241 ValArgGlyAenGlyPheArgHisAlaArgAenValAspArgValLeuCySerPheLys 260  
 DB 864 GTGAGAGGAAACGGCTTCCGACATGCCCCGCAACGTGACAGGGTCTCTGACGCTTCAAG 923  
 QY 261 ILeaAenAspSerValThrLeuAenGlyLysProPheSerValGluAspThrTyrLeuLeu 280  
 DB 924 ATCAATGACTCGGTCACTCACTCAATGAGAAAGCCCTTTCTGTGAGAGACACTTATTACTG 983  
 QY 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAen 300  
 DB 984 TGTCCAGCGCCCTATCTTAAAGAGTTGGCATGAAGCTGCACCTCCAGTCAGCATGAAAC 1043  
 QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrThiCysSerAspGly 320  
 DB 1044 GATGCGCTCTCTTTATCTCCAGTTCTGTCATCATCACCAACACACACTGTTCTGACGGT 1103  
 QY 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTrp 340  
 DB 1104 TCCATCTCGGCGCATGCGCCCTGCTGATCCTGTTCTGCTCCTAGCCCTGGCTCTCTGCG 1163  
 QY 341 TrpPheTrpProLeuCyCysThrValIleIleLysGluValProProProAlaGlu 360  
 DB 1164 TGGTTCTGGCCCTCTGCTGCACTGTGATTATCAAGAGGTCCCTCCACCCCTGCGAG 1223  
 QY 361 GluSerGluGlu 364  
 DB 1224 GAGAGTGAGGAA 1235

RESULT 12  
 US-10-038-307-17

; Sequence 17, Application US/10038307  
 ; Publication No. US20030134786A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: James B. ROTHMAN  
 ; APPLICANT: Theresa L. O'KEEFE  
 ; APPLICANT: Engin OKAYMAK

```
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 1674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-17

Alignment Scores:
Pred. No.: 1,076-151      Length: 1674
Score: 1661.00           Matches: 361
Percent Similarity: 67.54% Conservative: 26
Best Local Similarity: 63.00% Mismatches: 81
Query Match: 54.91%      Indels: 107
DB: 15                   Gaps: 12

US-09-970-076-6 (1-564) x US-10-038-307-17 (1-1674)

Oy      1 MetAlaThrAlaIleGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr
Db      13 ATGGCCAGCGGCGAGCGAGAGCCCTCGGCGATCGGCTTCCAGTGGCTCTTTGGCCACT
Oy      21 LeuValIleuIleCyAlaIleGlyIleGlyArgAlaGluArgGlyProAlaCysIleTy
Db      73 CTGGGCTCATCTGCGCGGCGAGCGAGCGAGAGAGGGGGTCCAGCCCTGCTAC
Oy      41 GlyGlyPheAspLeuTyPheIleLeuAspLysSerGlySerValIleuHisIleTrpAsn
Db      133 GCGCGATTTGACCTTACTTCTTTCGACAAATCAGAAAGTCTGCAACCTGGAT
Oy      61 GlnIleTyTyPheValIleGluIleuAlaHisLysPheIleSerProGlnLeuArgIle
Db      193 GAAATCTATTACTTGTGGACAGTTGGCTCACAATTCATCAGCCCAAGTTGAGATG
Oy      81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu
Db      253 TCCCTTATTGTTTCTCCACCCGAGGAACCACTTAATGAACCTGACAGAAACAGAA
Oy      101 GlnIleArgGlnGlyLeuGluIleuGlnLysValIleuProGlyGlyAspThrTyMet
Db      313 CAATTCCTGCAAGGCTTGAAGAACTCCAGAAAGTCTGCCAGAGGAGACACTTACATG
Oy      121 HisGluGlyPheGluArgAlaSerGluGlnIleTyTyGluAsnArgGlnGlyTyArg
Db      373 CATGAAGATTGGAAGGCGCCAGTGAAGATTTATGAAAACAGACAAAGGTTACAG
Oy      141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTy
Db      433 ACAGCAGCGCATCATATGCTTGTGACTGATGGAAGATCCCATGAAGATCTCTTTTTCAT
Oy      161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyTyCysValGlyAla
Db      493 TCAGAGAGGAGGCTTAATAGTCTGAGATCTTGGTGCATTTGTTTACTGTGTTGGTGG
Oy      181 LysAspPheAsnGlyThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro
Db      553 AAAAGATTCATGAGACACAGCTGGCCGGAATTCGAGACATGATCATGTGTTTCC
Oy      201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys
Db      613 GTGAATGAGCGCTTTCAGGCTCTGCAAGGCATCATCTCAATTTTGAAGAGTCCCTGC
Oy      221 IleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnValAla
Db      673 ATCGAAATTTCTGACGCTGAACCATCCACATATGTGACGAGATCATTTCAATTTGTC
Oy      241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValIleuCysSerPheLys
```

```
Db      792 GTGAGAGAAACGGCTTCCGACATGCCCGCAGGTGACAGGGTCTCTCGACCTTCAAG
Oy      261 IleAsnAspSerValThrLeuAsnGluValProPheSerValGluAspTrpTyLeuLeu
Db      793 ATCATATCTCGGCTACACTCAATGAGAGCCCTTTCTGTGGAGATCTTATTCTG
Oy      281 CysProAlaProIleLeuLysGluValAlaIleMetLysAlaAlaLeuGlnValSerMetAsn
Db      853 TGTCCAGCGCTATCTTAAGAAAGATTGGCATGAAGCTGACATCCAGCTCAGCATGAAAC
Oy      301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly
Db      913 GATGGCTCTCTTTATCTCAGTTCTGTCATCATCACACACACTGTTCTGACGGT
Oy      321 -----SerIleLeuAla 324
Db      973 CCCAAATCTTCTGACAAACTCACACATGCCACCGGCCAGCCTGAATCTGGCGGG
Oy      325 IleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTrpTrpPheTrpPro
Db      1033 GCACCGTCAGTCTTCTCTTC-----
Oy      345 LeuCysCysThrValIleIleLysGluValProProProProAlaGlu-----
Db      1054 -----CCCCAAACCCAGGACACCTTCATGATC 1083
Oy      361 -----GluSerGluGluAspAspGly 369
Db      1084 TCCCGGACCCCTGAGTCAATGCGTGTGTGTGAGTGTGAGCCAGAAAGC-----
Oy      370 LeuProLysLysTrpTrpProThrValAspAlaSerTyTyGlyGlyArg-----
Db      1135 -----CTGAGGTCAAGTTCAACTGATGATCGT- GGAACGGCGTGAAGT 1175
Oy      387 -----GlyValGlyGlyIleLysArgMetGluValArgTrpGlyGlu 400
Db      1176 GCATTAATCCCAAGCAAAAGCCGCGGAGGAGCAGTMCACAGCAGTACGTGTGTGAC
Oy      401 Lys-----GlySerThrGlu-----GluGlyAlaLysLeuGluLysAla 413
Db      1236 CGTCTCACCCTCTGTCACAGAGCTGGCTGAATGGCAAGGAGTACAAAGTCAAGTCTC
Oy      414 LysAsnAlaArgValLysMetProGluGlnGlyTrpIleuPheProArgAsnLeu 433
Db      1296 CAACAAAGC---CCTCCAGCCCCATCGAAGAAACCATCT- CCAAGCCAAAGCGCAGC 1351
Oy      434 AsnAsnAsnMetArgArgProSerSerProArgLysTrpTySer---ProIleLysGly 452
Db      1352 CCCGAGAACCAACAGTGTACACCTGCCCATCCCGGATGAGCTGACCAAGAACAGC 1411
Oy      453 LysLeuAspAlaLeuTrpValIleuLeuArgLysGlyTyArgAspArgValSerValMetArg 472
Db      1412 TCAGCTGACCTGCTG-----TCMAAGCTTCTATCTCCAGCG 1450
Oy      473 ProGlnProGlyAspTrpGlyArgCysIleAsnPheThrArgValLysAsnAsnGlnPro 492
Db      1451 ACATCGCGGTGG---ACTGGAGAGCAATGGAGCGCAGAG----- 1489
Oy      493 AlaLysTyTrpLeuAsnAsnAlaTyHisThrSerSerProProProAlaProIleTy 512
Db      1490 -----ACAACTCAAGAACCAACCGCTCCCGTGTGG 1519
Oy      513 ThrProProProProAlaProHisCysProProProPro 525
Db      1520 ACTCGACGGCTCTTCTCTCTCTTCAACAGAACTCACCG 1558

RESULT 13
US-10-201-292-17
; Sequence 17, Application US/10201292
; Publication No. US20030141193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
```

```

; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 1674
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-201-292-17

Alignment Scores:
Pred. No.: 1,076-151 Length: 1674
Score: 1661.00 Matches: 361
Percent Similarity: 67.54% Conservative: 26
Best Local Similarity: 63.00% Mismatches: 81
Query Match: 54.91% Indels: 107
DB: 15 Gaps: 12

US-09-970-076-6 (1-564) x US-10-201-292-17 (1-1674)
QY 1 MetAlaThrAlAGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
DB 13 ATGGCCACCGCGGAGCGGAGAGCCCTCGGCATCGGCTTCAGTGGCTCTCTTGGCCACT 72
QY 21 LeuValIleuIleCyseAlaGlyGlnGlyArgArgGluAspGlyGlyProAlaCyseTr 40
DB 73 CTGGTGCTCATCTGCGCCGCGGAGGAGGAGCGAGGAGAGATGGGGGTCCAGCTGCTAC 132
QY 41 GlyGlyPheAspLeuTrpThrIleLeuAspGlySerGlySerValLeuHisStrpAsn 60
DB 133 GCGGAGTTTGACCTGTAATCTCAATTTGACCAATCAGAAAGTGCTGTCACCACTGGAT 192
QY 61 GluIleTrpTrpPheValAGluGlnLeuAlaHisIleValPheIleSerProGlnLeuArgMet 80
DB 139 GAAATCTAATCTTGTGGAAAGCTTGGCTCACAAAATTCATCAGCCCAAGTTGAGAAATG 252
QY 81 SerPheIleValPheSerThrArgGlyTrpThrLeuMetIleLeuThrGluAspArgGlu 100
DB 253 TCCTTATATTGTTTCCACCCGAGGAAACACCTTAATGAACTGACAGAGACAGAGA 312
QY 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnIleValLeuProGlyGlyAspThrTrpMet 120
DB 313 CAATTCCTGCAAGGCTTACAGAAACTCCAGAAAGTTCTGCCAGGAGGACACTTACATG 372
QY 121 HisGluGlyPheGluArgAlaSerGluGlnIleTrpTrpGluAspArgGlnGlyTrpArg 140
DB 373 CATGAAAGATTGAAAGGCGCAGTGAGCATTTATTATGAAACAGACAGAGGATACAGG 432
QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGlyAspLeuPhePheTr 160
DB 433 ACAGCAGAGGTATATCTTCTTGAATGAGAACTCATGAGAAATCTCTTTTCTCAT 492
QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTrpCyseValGlyVal 180
DB 493 TCAGAGAGAGGAGGCTAATAGCTCTCGAATCTTGGGCAATTTGTTTAACTGTTGGTGG 552
QY 181 LysAspPheAsnGluTrpGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
DB 553 AAAGATTTCATGAGACACAGCTGGCCCGAATTGGGACAGTAAAGATATATGTTTCCC 612
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCy 220
DB 613 GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCTCAATTTTGAAGAAGTCTTCC 672
QY 221 IleGluIleLeuAlaIleGluProSerThrIleCyseAlaGlyGluSerPheGlnValVal 240
DB 673 ATCGAAATCTTACAGCTACCAATCCATATATGCGAGGAGATCATTTTAAAGTTGTC 732
QY 241 ValArgGlyAsnGlyPheArgHisAlaIleAsnValAspArgValLeuCyseSerPheLys 260

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DB 723 GTGAGAGAAAGCGCTTCAGACATCCCGCAACGTGACAGGCTCTCGACGTTCAAG 792
QY 261 IleAsnAspSerValThrLeuAsnGlyLysProPheSerValGluAspThrTrpLeuLeu 280
DB 793 ATCAATGACTCGGTACACTCAATGAGAAAGCCCTTTCTGGAGAAATATATTATCTG 852
QY 281 CysProAlaProIleLeuLysGluValAGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
DB 853 TGTCCAGGCGCTATTTAAAGAGTGTGCATGAAAGTGCCTCAGGTGACGTGAGTAAAC 912
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrTrpHisCyseSerAspGly 320
DB 913 GATGCGCTCTCTTTATCTTCAGTCTCTCATCATCACACACACACTGTTCTACCGT 972
QY 321 -----SerIleLeuAla 324
DB 973 CCCAAATCTTGCACAAACTCACACATGCCACCGTCCCGACACTGAACTCCGAGG 1032
QY 325 IleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTrpTrpPheTrpPro 344
DB 1033 GCACCGTCAAGTCTCTCTTC----- 1053
QY 345 LeuCyseCysThrValIleIleIleGluValProProProAlaGlu----- 360
DB 1054 -----CCCCAAACCCAGAGACACCTCATGATC 1083
QY 361 -----GluSerGluGluAspAspGly 369
DB 1084 TCCCGGACCCCTGAGGTCAATGCGGTGGTGAGCGAGCCAGACAGAAAGAC----- 1134
QY 370 LeuProLysLysTrpProThrValAspAlaSerTrpTrpGlyGlyArg----- 386
DB 1135 -----CTGAGGTCAAGTTCAACTGTGAGCT-GAGCGGGTGAAGT 1175
QY 387 -----GlyValGlyIleLysValGlyMetGluValArgTrpGlyGlu 400
DB 1176 GCATTAATGCCAAGAAACCGCGGAGAGAGACAGTACAAACAGCTACCGTGTGTGAG 1235
QY 401 Lys-----GlySerThrGlu--GluGlyAlaLysLeuGlnLysAla 413
DB 1236 CGTCTTCAACGTCCTGCACACAGACTGCTGATGCAAGAGTCAAGTCAAGTGTCTC 1295
QY 414 LysAsnAlaArgValLysMetProGluGlnGlyTrpGluPheProGluProArgAsnLeu 433
DB 1296 CAACAAGC---CTCCAGCGCCCATGAGAAACCATCT-CCAAAGCCAAAGGGCAGC 1351
QY 434 AsnAsnAsnMetArgArgProSerSerProArgLysTrpTrpTrpSer---ProIleLysGly 452
DB 1352 CCCGAAACACAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACAGG 1411
QY 453 LysLeuAspAlaLeuTrpValLeuLeuArgLysGlyTrpAspArgValSerValMetArg 472
DB 1412 TCAGCTGACCTGCTG-----TCAAGGCTTATATCCACAGG 1450
QY 473 ProGlnProGlyAspThrGlyArgCysIleAsnPheThrArgValLysAsnAsnGlnPro 492
DB 1451 ACATGCGCGTGG---AGTGGAGAGCAATGAGCAGCCGAGAG----- 1489
QY 493 AlaLysTrpProLeuAsnAlaValTrpHisIleSerSerProProAlaProIleTrp 512
DB 1490 -----ACAACTTCAAGAACCAACCGCTCCCGTGTGG 1519
QY 513 ThrProProProAlaProHisCyseArgProProProPro 525
DB 1520 ACTCGAGCGGCTCTTCTTCTCTTACAGCAAGCTCAGCG 1558

RESULT 14
US-10-038-307-15
; Sequence 15, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN

```



```

APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKANYNK
APPLICANT: Judith J. HEMLEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 1650
TYPE: DNA
ORGANISM: Homo sapiens
US-10-201-292-15

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Alignment Scores:		
Pred. No.:	7,066-151	Length: 1650
Score:	1652.50	Matches: 361
Percent Similarity:	67.78%	Conservative: 26
Best Local Similarity:	63.22%	Mismatches: 81
Query Match:	54.63%	Indels: 105
DB:	15	Gaps: 12

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: June 21, 2004, 13:44:26 ; Search time 33.2326 Seconds  
(without alignment)  
2828.859 Million cell updates/sec

Title: US-09-970-076-8

Perfect score: 1728

Sequence: 1 MATERRALGIGFQWLSLAT.....TTHCSLHKIASGPTTAACME 333

## Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09C\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of residues predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1728	100.0	333	10	US-09-796-753-12
2	1728	100.0	333	14	US-10-038-307-2
3	1728	100.0	333	14	US-10-201-292-2
4	1728	100.0	564	14	US-10-038-307-20
5	1728	100.0	564	14	US-10-201-292-20
6	1718	99.4	345	14	US-10-038-307-24
7	1718	99.4	345	14	US-10-201-292-24
8	1713.5	99.2	342	14	US-10-038-307-22
9	1713.5	99.2	342	14	US-10-201-292-22
10	1650.5	95.5	551	14	US-10-038-307-18
11	1650.5	95.5	551	14	US-10-201-292-18
12	1649	95.4	403	11	US-09-833-245-621
13	1649	95.4	564	12	US-09-918-715-187
14	1649	95.4	564	12	US-09-918-715-232
15	1649	95.4	564	14	US-10-301-822-199

16	1649	95.4	564	16	US-10-408-765A-1823	Sequence 1823, App
17	1644	95.1	403	11	US-09-833-245-620	Sequence 620, App
18	1636	94.7	328	14	US-10-038-307-26	Sequence 26, App
19	1636	94.7	328	14	US-10-201-292-26	Sequence 26, App
20	1628	94.2	543	14	US-10-038-307-14	Sequence 14, App
21	1628	94.2	543	14	US-10-038-307-16	Sequence 16, App
22	1628	94.2	543	14	US-10-201-292-14	Sequence 14, App
23	1628	94.2	543	14	US-10-201-292-16	Sequence 16, App
24	1618	93.6	543	14	US-10-038-307-10	Sequence 10, App
25	1618	93.6	543	14	US-10-201-292-10	Sequence 10, App
26	1556	90.0	529	14	US-10-201-292-36	Sequence 36, App
27	1553	89.9	562	12	US-09-918-715-194	Sequence 194, App
28	1553	89.9	562	12	US-09-918-715-301	Sequence 301, App
29	1487	86.1	534	14	US-10-038-307-12	Sequence 12, App
30	1487	86.1	534	14	US-10-201-292-12	Sequence 12, App
31	1434.5	83.0	504	14	US-10-201-292-32	Sequence 32, App
32	1307	75.6	479	14	US-10-201-292-32	Sequence 32, App
33	1193	69.0	460	14	US-10-201-292-28	Sequence 28, App
34	1183	68.5	460	14	US-10-201-292-30	Sequence 30, App
35	903	52.3	538	13	US-10-047-542-99	Sequence 99, App
36	800.5	46.3	488	10	US-09-796-753-52	Sequence 52, App
37	800.5	46.3	488	14	US-10-038-307-6	Sequence 6, App
38	800.5	46.3	488	14	US-10-201-292-6	Sequence 6, App
39	800.5	46.3	488	14	US-10-368-087-16	Sequence 16, App
40	800.5	46.3	488	15	US-10-104-047-2639	Sequence 2639, App
41	785.5	45.5	587	9	US-09-764-870-312	Sequence 312, App
42	785.5	45.5	587	11	US-09-764-875-968	Sequence 968, App
43	785.5	45.5	587	14	US-10-125-540-312	Sequence 312, App
44	771	44.6	487	10	US-09-796-753-54	Sequence 54, App
45	771	44.6	487	14	US-10-038-307-8	Sequence 8, App

## ALIGNMENTS

RESULT 1  
US-09-796-753-12  
Sequence 12, Application US/09796753  
Publication No. US20030027998A1  
GENERAL INFORMATION:  
APPLICANT: McCarthy, Sean A.  
TITLE OF INVENTION: SECRETED PROTEINS AND USRS THEREOF  
FILE REFERENCE: 7853-227-999  
CURRENT APPLICATION NUMBER: US/09/796,753  
CURRENT FILING DATE: 2001-03-01  
PRIOR APPLICATION NUMBER: 09/183,175  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: 09/223,094  
PRIOR FILING DATE: 1998-12-30  
PRIOR APPLICATION NUMBER: 09/223,546  
PRIOR FILING DATE: 1998-12-30  
PRIOR APPLICATION NUMBER: 09/224,246  
PRIOR FILING DATE: 1998-12-30  
PRIOR APPLICATION NUMBER: 09/259,388  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: 60/122,458  
PRIOR FILING DATE: 1999-03-01  
PRIOR APPLICATION NUMBER: 09/312,359  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 09/336,536  
PRIOR FILING DATE: 1999-06-18  
PRIOR APPLICATION NUMBER: 09/342,687  
PRIOR FILING DATE: 1999-06-29  
PRIOR APPLICATION NUMBER: 09/345,464  
PRIOR FILING DATE: 1999-06-30  
PRIOR APPLICATION NUMBER: 09/365,164  
PRIOR FILING DATE: 1999-07-30  
PRIOR APPLICATION NUMBER: 09/399,723  
PRIOR FILING DATE: 1999-09-20  
PRIOR APPLICATION NUMBER: 09/409,634  
PRIOR FILING DATE: 1999-09-30  
PRIOR APPLICATION NUMBER: 09/471,179  
PRIOR FILING DATE: 1999-12-23

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; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
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; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 12
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-753-12

```

```

Query Match      100.0%; Score 1728; DB 10; Length 333;
Best Local Similarity 100.0%; Pred. No. 4.3e-175;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPAACGFGDLYFLDKSGSVLHHMN 60
      1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPAACGFGDLYFLDKSGSVLHHMN 60
DB      1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPAACGFGDLYFLDKSGSVLHHMN 60
QY      61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDREQIRGLBELQKVLPGDPTM 120
      61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDREQIRGLBELQKVLPGDPTM 120
DB      61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDREQIRGLBELQKVLPGDPTM 120
QY      121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSRDIGAIYVCYGV 180
      121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSRDIGAIYVCYGV 180
DB      121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSRDIGAIYVCYGV 180
QY      121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSRDIGAIYVCYGV 180
      121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSRDIGAIYVCYGV 180
DB      121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSRDIGAIYVCYGV 180
QY      181 KDFNETQLARIADSKDHPVNDGFQALOGIHSILKSCIEILAAEPSTICAGESFOVV 240
      181 KDFNETQLARIADSKDHPVNDGFQALOGIHSILKSCIEILAAEPSTICAGESFOVV 240
DB      181 KDFNETQLARIADSKDHPVNDGFQALOGIHSILKSCIEILAAEPSTICAGESFOVV 240
QY      241 VRGNFRRARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300
      241 VRGNFRRARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300
DB      241 VRGNFRRARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300
QY      301 DGLSFISSSVIITTHCSLHKIASGPTTAACME 333
      301 DGLSFISSSVIITTHCSLHKIASGPTTAACME 333
DB      301 DGLSFISSSVIITTHCSLHKIASGPTTAACME 333

```

```

RESULT 2
US-10-038-307-2
; Sequence 2, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038.307
; CURRENT FILING DATE: 2002-06-28

```

```

; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-2

```

```

Query Match      100.0%; Score 1728; DB 14; Length 333;
Best Local Similarity 100.0%; Pred. No. 4.3e-175;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPAACGFGDLYFLDKSGSVLHHMN 60
      1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPAACGFGDLYFLDKSGSVLHHMN 60
DB      1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPAACGFGDLYFLDKSGSVLHHMN 60
QY      61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDREQIRGLBELQKVLPGDPTM 120
      61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDREQIRGLBELQKVLPGDPTM 120
DB      61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDREQIRGLBELQKVLPGDPTM 120
QY      121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSRDIGAIYVCYGV 180
      121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSRDIGAIYVCYGV 180
DB      121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSRDIGAIYVCYGV 180
QY      121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSRDIGAIYVCYGV 180
      121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSRDIGAIYVCYGV 180
DB      121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSRDIGAIYVCYGV 180
QY      241 VRGNFRRARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300
      241 VRGNFRRARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300
DB      241 VRGNFRRARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300
QY      301 DGLSFISSSVIITTHCSLHKIASGPTTAACME 333
      301 DGLSFISSSVIITTHCSLHKIASGPTTAACME 333
DB      301 DGLSFISSSVIITTHCSLHKIASGPTTAACME 333

```

```

RESULT 3
US-10-201-292-2
; Sequence 2, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201.292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-2

```

```

Query Match      100.0%; Score 1728; DB 14; Length 333;
Best Local Similarity 100.0%; Pred. No. 4.3e-175;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPAACGFGDLYFLDKSGSVLHHMN 60
      1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPAACGFGDLYFLDKSGSVLHHMN 60
DB      1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPAACGFGDLYFLDKSGSVLHHMN 60
QY      61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDREQIRGLBELQKVLPGDPTM 120
      61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDREQIRGLBELQKVLPGDPTM 120
DB      61 EIIYFVEQLAHKFIISPOLRMSFIVFSTRGTTLMKLTEDREQIRGLBELQKVLPGDPTM 120
QY      121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSRDIGAIYVCYGV 180
      121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSRDIGAIYVCYGV 180
DB      121 HEGFERASEQIYYENRQGYRTASVITALTGELHEDLFFYSERANRSRDIGAIYVCYGV 180

```



QY 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIITHSLIKKSCIEIILAEPSSTICAGSFOVY 240  
 DB 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIITHSLIKKSCIEIILAEPSSTICAGSFOVY 240  
 QY 241 VRGNCFRARIANDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKMAALQVSMN 300  
 DB 241 VRGNCFRARIANDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKMAALQVSMN 300  
 QY 301 DGLSPFISSSVIITTHCSLHKIASGPTTAACME 333  
 DB 301 DGLSPFISSSVIITTHCSLHKIASGPTTAACME 333

#### RESULT 4

US-10-038-307-20  
 ; Sequence 20, Application US/10038307  
 ; Publication No. US20030134786A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: James B. ROTTMAN  
 ; APPLICANT: Theresa L. O'KEEFE  
 ; APPLICANT: Engin OZKAYNAK  
 ; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
 ; FILE REFERENCE: 7853-253-999  
 ; CURRENT APPLICATION NUMBER: US/10/038,307  
 ; CURRENT FILING DATE: 2002-06-28  
 ; NUMBER OF SEQ ID NOS: 26  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 20  
 ; LENGTH: 564  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-038-307-20

Query Match 100.0%; Score 1728; DB 14; Length 564;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-175;  
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATERRALGIGFQWLSLATLVLCAGGCGRRBDGPACYGFDLYFILDKSGSVLHHMN 60  
 DB 1 MATERRALGIGFQWLSLATLVLCAGGCGRRBDGPACYGFDLYFILDKSGSVLHHMN 60  
 QY 61 EIIYFVEQLAHKFTSPQLRMSFIVSTRTGTTLMKLTEDREQIROLLELOKVLPGGDTYM 120  
 DB 61 EIIYFVEQLAHKFTSPQLRMSFIVSTRTGTTLMKLTEDREQIROLLELOKVLPGGDTYM 120  
 QY 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYCYGV 180  
 DB 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYCYGV 180  
 QY 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIITHSLIKKSCIEIILAEPSSTICAGSFOVY 240  
 DB 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIITHSLIKKSCIEIILAEPSSTICAGSFOVY 240  
 QY 241 VRGNCFRARIANDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKMAALQVSMN 300  
 DB 241 VRGNCFRARIANDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKMAALQVSMN 300  
 QY 301 DGLSPFISSSVIITTHCSLHKIASGPTTAACME 333  
 DB 301 DGLSPFISSSVIITTHCSLHKIASGPTTAACME 333

#### RESULT 5

US-10-201-292-20  
 ; Sequence 20, Application US/10201292  
 ; Publication No. US2003014193A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: James B. ROTTMAN  
 ; APPLICANT: Theresa L. O'KEEFE  
 ; APPLICANT: Engin OZKAYNAK  
 ; APPLICANT: Judith J. HEALEY

; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
 ; FILE REFERENCE: 7853-253-999  
 ; CURRENT APPLICATION NUMBER: US/10/201,292  
 ; CURRENT FILING DATE: 2003-02-14  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 20  
 ; LENGTH: 564  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-201-292-20

Query Match 100.0%; Score 1728; DB 14; Length 564;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-175;  
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATERRALGIGFQWLSLATLVLCAGGCGRRBDGPACYGFDLYFILDKSGSVLHHMN 60  
 DB 1 MATERRALGIGFQWLSLATLVLCAGGCGRRBDGPACYGFDLYFILDKSGSVLHHMN 60  
 QY 61 EIIYFVEQLAHKFTSPQLRMSFIVSTRTGTTLMKLTEDREQIROLLELOKVLPGGDTYM 120  
 DB 61 EIIYFVEQLAHKFTSPQLRMSFIVSTRTGTTLMKLTEDREQIROLLELOKVLPGGDTYM 120  
 QY 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYCYGV 180  
 DB 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYCYGV 180  
 QY 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIITHSLIKKSCIEIILAEPSSTICAGSFOVY 240  
 DB 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIITHSLIKKSCIEIILAEPSSTICAGSFOVY 240  
 QY 241 VRGNCFRARIANDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKMAALQVSMN 300  
 DB 241 VRGNCFRARIANDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKMAALQVSMN 300  
 QY 301 DGLSPFISSSVIITTHCSLHKIASGPTTAACME 333  
 DB 301 DGLSPFISSSVIITTHCSLHKIASGPTTAACME 333

#### RESULT 6

US-10-038-307-24  
 ; Sequence 24, Application US/10038307  
 ; Publication No. US20030134786A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: James B. ROTTMAN  
 ; APPLICANT: Theresa L. O'KEEFE  
 ; APPLICANT: Engin OZKAYNAK  
 ; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
 ; FILE REFERENCE: 7853-253-999  
 ; CURRENT APPLICATION NUMBER: US/10/038,307  
 ; CURRENT FILING DATE: 2002-06-28  
 ; NUMBER OF SEQ ID NOS: 26  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 24  
 ; LENGTH: 345  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-038-307-24

Query Match 99.4%; Score 1718; DB 14; Length 345;  
 Best Local Similarity 99.7%; Pred. No. 5.3e-174;  
 Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATERRALGIGFQWLSLATLVLCAGGCGRRBDGPACYGFDLYFILDKSGSVLHHMN 60  
 DB 1 MATERRALGIGFQWLSLATLVLCAGGCGRRBDGPACYGFDLYFILDKSGSVLHHMN 60  
 QY 61 EIIYFVEQLAHKFTSPQLRMSFIVSTRTGTTLMKLTEDREQIROLLELOKVLPGGDTYM 120  
 DB 61 EIIYFVEQLAHKFTSPQLRMSFIVSTRTGTTLMKLTEDREQIROLLELOKVLPGGDTYM 120

QY 121 HEGFERASEQIYENROGYRTASVIALTDGELHEDLFFYSEBRANRSDIGAIYVCV 180  
 DB 121 HEGFERASEQIYENROGYRTASVIALTDGELHEDLFFYSEBRANRSDIGAIYVCV 180  
 QY 181 KDFNETOLARIADSKDHVPVNDGFOALOGIHSILKSCIEIIAABSTICAGESFOV 240  
 DB 181 KDFNETOLARIADSKDHVPVNDGFOALOGIHSILKSCIEIIAABSTICAGESFOV 240  
 QY 241 VRGNGFRHARVNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300  
 DB 241 VRGNGFRHARVNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300  
 QY 301 DGLSFISISSVITTTTCHSLHKLASGPTTAACME 333  
 DB 301 DGLSFISISSVITTTTCHSLHKLASGPTTAACME 333

# RESULT 7

US-10-201-292-24  
 ; Sequence 24, Application US/10201292  
 ; Publication No. US20030144193A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: James B. ROTTMAN  
 ; APPLICANT: Theresa L. O'KEEFE  
 ; APPLICANT: Engin OZKAYNAK  
 ; APPLICANT: Judith J. HEALEY  
 ; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
 ; FILE REFERENCE: 7853-253-999  
 ; CURRENT APPLICATION NUMBER: US/10/201.292  
 ; CURRENT FILING DATE: 2003-02-14  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 24  
 ; LENGTH: 345  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-201-292-24

Query Match 99.4%; Score 1718; DB 14; Length 345;

Best Local Similarity 99.7%; Pred. No. 5.3e-174; Indels 0; Gaps 0;  
 Matches 332; Conservative 0; Mismatches 1;

QY 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGPGACGFDLYFILDKSGSVLHHMN 60  
 DB 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGPGACGFDLYFILDKSGSVLHHMN 60  
 QY 61 EIIYFVEQLAHKFISPOLRMSFIVFSTRGTTLMKLTEDREQIROGLEELQVLPFGDTYM 120  
 DB 61 EIIYFVEQLAHKFISPOLRMSFIVFSTRGTTLMKLTEDREQIROGLEELQVLPFGDTYM 120  
 QY 121 HEGFERASEQIYENROGYRTASVIALTDGELHEDLFFYSEBRANRSDIGAIYVCV 180  
 DB 121 HEGFERASEQIYENROGYRTASVIALTDGELHEDLFFYSEBRANRSDIGAIYVCV 180  
 QY 181 KDFNETOLARIADSKDHVPVNDGFOALOGIHSILKSCIEIIAABSTICAGESFOV 240  
 DB 181 KDFNETOLARIADSKDHVPVNDGFOALOGIHSILKSCIEIIAABSTICAGESFOV 240  
 QY 241 VRGNGFRHARVNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300  
 DB 241 VRGNGFRHARVNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300  
 QY 301 DGLSFISISSVITTTTCHSLHKLASGPTTAACME 333  
 DB 301 DGLSFISISSVITTTTCHSLHKLASGPTTAACME 333

# RESULT 8

US-10-038-307-22  
 ; Sequence 22, Application US/10038307  
 ; Publication No. US20030134786A1  
 ; GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN  
 APPLICANT: Theresa L. O'KEEFE  
 APPLICANT: Engin OZKAYNAK  
 APPLICANT: Judith J. HEALEY  
 TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
 FILE REFERENCE: 7853-253-999  
 CURRENT APPLICATION NUMBER: US/10/038.307  
 CURRENT FILING DATE: 2002-06-28  
 NUMBER OF SEQ ID NOS: 26  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 22  
 LENGTH: 342  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-038-307-22

Query Match 99.2%; Score 1713.5; DB 14; Length 342;  
 Best Local Similarity 97.4%; Pred. No. 1.6e-173;  
 Matches 333; Conservative 0; Mismatches 0; Indels 9; Gaps 1;

QY 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGPGACGFDLYFILDKSGSVLHHMN 60  
 DB 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGPGACGFDLYFILDKSGSVLHHMN 60  
 QY 52 SGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVFSTRGTTLMKLTEDREQIROGLEELQV 111  
 DB 52 SGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVFSTRGTTLMKLTEDREQIROGLEELQV 111  
 QY 61 SGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVFSTRGTTLMKLTEDREQIROGLEELQV 120  
 DB 61 SGSVLHHMNEIYFVEQLAHKFISPOLRMSFIVFSTRGTTLMKLTEDREQIROGLEELQV 120  
 QY 112 VLPFGDTYMHEGFERASEQIYENROGYRTASVIALTDGELHEDLFFYSEBRANRSD 171  
 DB 112 VLPFGDTYMHEGFERASEQIYENROGYRTASVIALTDGELHEDLFFYSEBRANRSD 171  
 QY 121 VLPFGDTYMHEGFERASEQIYENROGYRTASVIALTDGELHEDLFFYSEBRANRSD 180  
 DB 121 VLPFGDTYMHEGFERASEQIYENROGYRTASVIALTDGELHEDLFFYSEBRANRSD 180  
 QY 172 GAIVYCVGNDPNETOLARIADSKDHVPVNDGFOALOGIHSILKSCIEIIAABSTI 231  
 DB 172 GAIVYCVGNDPNETOLARIADSKDHVPVNDGFOALOGIHSILKSCIEIIAABSTI 231  
 QY 181 GAIVYCVGNDPNETOLARIADSKDHVPVNDGFOALOGIHSILKSCIEIIAABSTI 240  
 DB 181 GAIVYCVGNDPNETOLARIADSKDHVPVNDGFOALOGIHSILKSCIEIIAABSTI 240  
 QY 232 CAGESFOVVRGNGFRHARVNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVG 291  
 DB 232 CAGESFOVVRGNGFRHARVNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVG 291  
 QY 241 CAGESFOVVRGNGFRHARVNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVG 300  
 DB 241 CAGESFOVVRGNGFRHARVNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVG 300  
 QY 292 KAALQVSMNDGLSFISISSVITTTTCHSLHKLASGPTTAACME 333  
 DB 292 KAALQVSMNDGLSFISISSVITTTTCHSLHKLASGPTTAACME 333  
 QY 301 KAALQVSMNDGLSFISISSVITTTTCHSLHKLASGPTTAACME 342  
 DB 301 KAALQVSMNDGLSFISISSVITTTTCHSLHKLASGPTTAACME 342

# RESULT 9

US-10-201-292-22  
 ; Sequence 22, Application US/10201292  
 ; Publication No. US20030144193A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: James B. ROTTMAN  
 ; APPLICANT: Theresa L. O'KEEFE  
 ; APPLICANT: Engin OZKAYNAK  
 ; APPLICANT: Judith J. HEALEY  
 ; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
 ; FILE REFERENCE: 7853-253-999  
 ; CURRENT APPLICATION NUMBER: US/10/201.292  
 ; CURRENT FILING DATE: 2003-02-14  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 22  
 ; LENGTH: 342  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-201-292-22

Query Match 99.2%; Score 1713.5; DB 14; Length 342;

Best Local Similarity 97.4%; Pred. No. 1.6e-173;  
 Matches 333; Conservative 0; Mismatches 0; Indels 9; Gaps 1;

QY 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGPGACGFDLYFILDKSGSVLHHMN 60  
 DB 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGPGACGFDLYFILDKSGSVLHHMN 60

```

QY 52 SGSVLHNNHNIYFVEQLAHKFIISPOLRMSPIVSTRTGTTLMKLTEDREQIQLGELQK 111
DB 61 SGSVLHNNHNIYFVEQLAHKFIISPOLRMSPIVSTRTGTTLMKLTEDREQIQLGELQK 120
QY 112 VLPQGDYTHHEGPERASEQIYYENRGYRTASVIALTDGELHEDLPFYSEERANRSD 171
DB 121 VLPQGDYTHHEGPERASEQIYYENRGYRTASVIALTDGELHEDLPFYSEERANRSD 180
QY 172 GAIYVCVGVKDNENETOLARIADSKOHVPVNDGFOALOGIHSILKSCIEIIAEPSTI 231
DB 181 GAIYVCVGVKDNENETOLARIADSKOHVPVNDGFOALOGIHSILKSCIEIIAEPSTI 240
QY 232 CAGESFOVYVVRNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGM 291
DB 241 CAGESFOVYVVRNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGM 300
QY 292 KALOVSNMNDGLSFISSSVITTTTHCSLHKIASGPTTAA 333
DB 301 KALOVSNMNDGLSFISSSVITTTTHCSLHKIASGPTTAA 342

```

# RESULT 10

```

US-10-038-307-18
; Sequence 18, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-18

```

Query Match 95.5%; Score 1650.5; DB 14; Length 551;  
 Best Local Similarity 97.3%; Pred. No. 1.7e-166;  
 Matches 320; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

```

QY 1 MATARRALGIGFOWLSLTLVLIICAGGGRREDGPAFCYGGFDLYFTLDKSGSVLHNN 60
DB 1 MATARRALGIGFOWLSLTLVLIICAGGGRREDGPAFCYGGFDLYFTLDKSGSVLHNN 60
QY 61 EIIYFVEQLAHKFIISPOLRMSPIVSTRTGTTLMKLTEDREQIQLGELQK 120
DB 61 EIIYFVEQLAHKFIISPOLRMSPIVSTRTGTTLMKLTEDREQIQLGELQK 120
QY 121 HEGFERASEQIYYENRGYRTASVIALTDGELHEDLPFYSEERANRSDCAIYVCV 180
DB 121 HEGFERASEQIYYENRGYRTASVIALTDGELHEDLPFYSEERANRSDCAIYVCV 180
QY 181 KOFNETOLARIADSKOHVPVNDGFOALOGIHSILKSCIEIIAEPSTICAGESFOV 240
DB 181 KOFNETOLARIADSKOHVPVNDGFOALOGIHSILKSCIEIIAEPSTICAGESFOV 240
QY 241 VRNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKALQVSN 300
DB 241 VRNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKALQVSN 300
QY 301 DGLSFISSSVITTTTHCSLHKIASGPTTAA 329
DB 301 DGLSFISSSVITTTTHCSLHKIASGPTTAA 324

```

RESULT 11

```

US-10-201-292-18
; Sequence 18, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKANAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-18

```

Query Match 95.5%; Score 1650.5; DB 14; Length 551;  
 Best Local Similarity 97.3%; Pred. No. 1.7e-166;  
 Matches 320; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

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QY 1 MATARRALGIGFOWLSLTLVLIICAGGGRREDGPAFCYGGFDLYFTLDKSGSVLHNN 60
DB 1 MATARRALGIGFOWLSLTLVLIICAGGGRREDGPAFCYGGFDLYFTLDKSGSVLHNN 60
QY 61 EIIYFVEQLAHKFIISPOLRMSPIVSTRTGTTLMKLTEDREQIQLGELQK 120
DB 61 EIIYFVEQLAHKFIISPOLRMSPIVSTRTGTTLMKLTEDREQIQLGELQK 120
QY 121 HEGFERASEQIYYENRGYRTASVIALTDGELHEDLPFYSEERANRSDCAIYVCV 180
DB 121 HEGFERASEQIYYENRGYRTASVIALTDGELHEDLPFYSEERANRSDCAIYVCV 180
QY 181 KOFNETOLARIADSKOHVPVNDGFOALOGIHSILKSCIEIIAEPSTICAGESFOV 240
DB 181 KOFNETOLARIADSKOHVPVNDGFOALOGIHSILKSCIEIIAEPSTICAGESFOV 240
QY 241 VRNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKALQVSN 300
DB 241 VRNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKALQVSN 300
QY 301 DGLSFISSSVITTTTHCSLHKIASGPTTAA 329
DB 301 DGLSFISSSVITTTTHCSLHKIASGPTTAA 324

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RESULT 12
US-09-833-245-621
; Sequence 621, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PFS46PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 621
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-621

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Query Match 95.4%; Score 1649; DB 11; Length 403;  
Best Local Similarity 100.0%; Pred. No. 1.5e-166;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPAICYGFDLYFLIDKSGSVLHHMN 60  
Db 1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPAICYGFDLYFLIDKSGSVLHHMN 60  
Qy 61 EIIYFVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTREDOIRQGLELOKVLPGSDTYM 120  
Db 61 EIIYFVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTREDOIRQGLELOKVLPGSDTYM 120  
Qy 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFYSEERANRSRDIGAIYVCYV 180  
Db 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFYSEERANRSRDIGAIYVCYV 180  
Qy 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIIHSILKSCIEIIAAEPSTICAGESFOVV 240  
Db 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIIHSILKSCIEIIAAEPSTICAGESFOVV 240  
Qy 241 VRNGGFHARNVDVRLCSFKINDSVTLNEKPFVSDTYLLCPAPILKEVGMKALQVSMN 300  
Db 241 VRNGGFHARNVDVRLCSFKINDSVTLNEKPFVSDTYLLCPAPILKEVGMKALQVSMN 300  
Qy 301 DGLSFSSSVIITTTTHCS 318  
Db 301 DGLSFSSSVIITTTTHCS 318

RESULT 13  
US-09-918-715-187  
; Sequence 187, Application US/09918715  
; Publication No. US20030017157A1  
; GENERAL INFORMATION:  
; APPLICANT: Brad St. Croix  
; APPLICANT: Bert Vogelstein  
; APPLICANT: Kenneth Kinzler  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00134  
; CURRENT APPLICATION NUMBER: US/09/918,715  
; CURRENT FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/222,599  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR APPLICATION NUMBER: 60/224,360  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 187  
; LENGTH: 564  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-918-715-187

Query Match 95.4%; Score 1649; DB 12; Length 564;  
Best Local Similarity 100.0%; Pred. No. 2.6e-166;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPAICYGFDLYFLIDKSGSVLHHMN 60  
Db 1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPAICYGFDLYFLIDKSGSVLHHMN 60  
Qy 61 EIIYFVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTREDOIRQGLELOKVLPGSDTYM 120  
Db 61 EIIYFVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTREDOIRQGLELOKVLPGSDTYM 120  
Qy 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFYSEERANRSRDIGAIYVCYV 180  
Db 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFYSEERANRSRDIGAIYVCYV 180  
Qy 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIIHSILKSCIEIIAAEPSTICAGESFOVV 240  
Db 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIIHSILKSCIEIIAAEPSTICAGESFOVV 240

Db 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIIHSILKSCIEIIAAEPSTICAGESFOVV 240  
Qy 241 VRNGGFHARNVDVRLCSFKINDSVTLNEKPFVSDTYLLCPAPILKEVGMKALQVSMN 300  
Db 241 VRNGGFHARNVDVRLCSFKINDSVTLNEKPFVSDTYLLCPAPILKEVGMKALQVSMN 300  
Qy 301 DGLSFSSSVIITTTTHCS 318  
Db 301 DGLSFSSSVIITTTTHCS 318

RESULT 14  
US-09-918-715-232  
; Sequence 232, Application US/09918715  
; Publication No. US20030017157A1  
; GENERAL INFORMATION:  
; APPLICANT: Brad St. Croix  
; APPLICANT: Bert Vogelstein  
; APPLICANT: Kenneth Kinzler  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00134  
; CURRENT APPLICATION NUMBER: US/09/918,715  
; CURRENT FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/222,599  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR APPLICATION NUMBER: 60/224,360  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 232  
; LENGTH: 564  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-918-715-232

Query Match 95.4%; Score 1649; DB 12; Length 564;  
Best Local Similarity 100.0%; Pred. No. 2.6e-166;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPAICYGFDLYFLIDKSGSVLHHMN 60  
Db 1 MATERRALGIGFQWLSLATTVLICAGGGRREDGPAICYGFDLYFLIDKSGSVLHHMN 60  
Qy 61 EIIYFVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTREDOIRQGLELOKVLPGSDTYM 120  
Db 61 EIIYFVEQLAHKFISPOLRMSFIVSTRTGTTLMKLTREDOIRQGLELOKVLPGSDTYM 120  
Qy 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFYSEERANRSRDIGAIYVCYV 180  
Db 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFYSEERANRSRDIGAIYVCYV 180  
Qy 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIIHSILKSCIEIIAAEPSTICAGESFOVV 240  
Db 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIIHSILKSCIEIIAAEPSTICAGESFOVV 240  
Qy 241 VRNGGFHARNVDVRLCSFKINDSVTLNEKPFVSDTYLLCPAPILKEVGMKALQVSMN 300  
Db 241 VRNGGFHARNVDVRLCSFKINDSVTLNEKPFVSDTYLLCPAPILKEVGMKALQVSMN 300  
Qy 301 DGLSFSSSVIITTTTHCS 318  
Db 301 DGLSFSSSVIITTTTHCS 318

RESULT 15  
US-10-301-822-199  
; Sequence 199, Application US/10301822  
; Publication No. US20030148410A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Berget, Allison

```

APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPM01-023922RNM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIORITY APPLICATION NUMBER: US 60/353,971
PRIORITY FILING DATE: 2001-12-10
PRIORITY APPLICATION NUMBER: US 60/361,978
PRIORITY FILING DATE: 2002-03-05
PRIORITY APPLICATION NUMBER: US 60/381,988
PRIORITY FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq For Windows Version 4.0
SEQ ID NO 199
LENGTH: 564
TYPE: PR1
ORGANISM: Homo Sapiens
US-10-301-822-199

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Result No.	Score	Query Match	Length	DB	ID	Description
1	3025	100.0	564	12	US-09-918-715-187	Sequence 187, App
2	3025	100.0	564	12	US-09-918-715-232	Sequence 232, App
3	3025	100.0	564	14	US-10-301-822-199	Sequence 199, App
4	3025	100.0	564	16	US-10-408-765A-1823	Sequence 1823, App
5	2901	95.9	562	12	US-09-918-715-194	Sequence 194, App
6	2901	95.9	562	12	US-09-918-715-301	Sequence 301, App
7	2017	66.7	381	10	US-09-796-753-24	Sequence 24, App1
8	2017	66.7	381	14	US-10-038-307-4	Sequence 4, App1
9	2017	66.7	381	14	US-10-201-292-4	Sequence 4, App1
10	1893.5	62.0	403	11	US-09-833-245-621	Sequence 621, App
11	1874	62.0	403	11	US-09-833-245-620	Sequence 620, App
12	1661	54.9	551	14	US-10-038-307-18	Sequence 18, App1
13	1661	54.9	551	14	US-10-201-292-18	Sequence 18, App1
14	1649	54.5	333	14	US-09-796-753-12	Sequence 12, App1
15	1649	54.5	333	14	US-10-038-307-2	Sequence 2, App1

16	1549	54.5	333	14	US-10-201-292-2	Sequence 2,	App1
17	1469	54.5	345	14	US-10-038-07-22	Sequence 24,	App1
18	1469	54.5	345	14	US-10-201-292-24	Sequence 24,	App1
19	1649	54.5	564	14	US-10-038-07-20	Sequence 20,	App1
20	1649	54.5	564	14	US-10-201-292-20	Sequence 20,	App1
21	1636	54.1	328	14	US-10-038-07-26	Sequence 26,	App1
22	1636	54.1	328	14	US-10-201-292-26	Sequence 26,	App1
23	1634.5	54.0	342	14	US-10-038-07-22	Sequence 22,	App1
24	1634.5	54.0	342	14	US-10-201-292-22	Sequence 22,	App1
25	1629	53.9	543	14	US-10-038-07-14	Sequence 14,	App1
26	1629	53.9	543	14	US-10-038-07-16	Sequence 16,	App1
27	1629	53.9	543	14	US-10-201-292-16	Sequence 16,	App1
28	1629	53.9	543	14	US-10-031-292-16	Sequence 16,	App1
29	1619	53.5	543	14	US-10-038-07-10	Sequence 10,	App1
30	1552.5	51.3	529	14	US-10-201-292-10	Sequence 10,	App1
31	1488	49.2	534	14	US-10-031-292-36	Sequence 36,	App1
32	1488	49.2	534	14	US-10-038-07-12	Sequence 12,	App1
33	1488	49.2	534	14	US-10-201-292-12	Sequence 12,	App1
34	1434.5	47.4	488	14	US-10-368-087-16	Sequence 16,	App1
35	1416.5	46.8	488	15	US-10-104-047-2639	Sequence 2639,	App1
36	1416.5	46.8	488	10	US-09-796-153-53	Sequence 53,	App1
37	1411.5	46.7	488	14	US-10-039-07-6	Sequence 6,	App1
38	1411.5	46.7	488	14	US-10-201-292-6	Sequence 6,	App1
39	1411.5	46.7	488	10	US-09-796-153-54	Sequence 54,	App1
40	1396.5	46.2	487	14	US-10-038-07-8	Sequence 8,	App1
41	1396.5	46.2	487	14	US-10-201-292-8	Sequence 8,	App1
42	1396.5	46.2	487	14	US-10-368-087-15	Sequence 15,	App1
43	1307	43.2	479	14	US-10-201-292-32	Sequence 32,	App1
45	1206.5	39.9	587	9	US-09-764-870-312	Sequence 312,	App1

## ALIGNMENTS

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RESULT 1
US-09-918-715-187
; Sequence 187, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918.715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,559
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 564
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-918-715-187

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Query Match	100.0%	Score 3025;	DB 12;	Length 564;
Best Local Similarity	100.0%	Pred. No. 3.7e-225;		
Matches 564; Conservative	0;	Mismatches	0;	Indels 0
				Gaps 0

OY	1	MATERRALGICFOWLSLATTVLICAGOGGRRDDGPAAYCGCFDLYF	11	LDKSGSVLAHNN	60
Db	1	MATERRALGICFOWLSLATTVLICAGOGGRRDDGPAAYCGCFDLYF	11	LDKSGSVLAHNN	60
OY	61	EIYYFEVLAKHFISSPOLRMSPIVSTRTGTLIMKLTEDREQIROGIEELQKYLPGGDTYV	120		
Db	61	EIYYFEVLAKHFISSPOLRMSPIVSTRTGTLIMKLTEDREQIROGIEELQKYLPGGDTYV	120		

Qy 121 HEGFERASEQIYYENRQGYRTASVIALITDGLHEDLFPYSERANRSDIGAIVYCVG 180  
Db 121 HEGFERASEQIYYENRQGYRTASVIALITDGLHEDLFPYSERANRSDIGAIVYCVG 180  
Qy 181 KDFNETOLARIADSKDHFVFNVDGFOALOGIISHILKSCIEILAAEPSTICAGESFOV 240  
Db 181 KDFNETOLARIADSKDHFVFNVDGFOALOGIISHILKSCIEILAAEPSTICAGESFOV 240  
Qy 241 VRNGGFHARNVDRVLCSPKINDSVTLNEKPFVSDTYLLCPAPILKEVGKALQVSMN 300  
Db 241 VRNGGFHARNVDRVLCSPKINDSVTLNEKPFVSDTYLLCPAPILKEVGKALQVSMN 300  
Qy 301 DGLSFSSSVIITTHCSDSIIAIALIIFLLAIALMLWFWPLCCTVIIKEVPPPAE 360  
Db 301 DGLSFSSSVIITTHCSDSIIAIALIIFLLAIALMLWFWPLCCTVIIKEVPPPAE 360  
Qy 361 ESEBEDDGLPKKMPITVDASYGGRGVGIIKMEVWGEKSTEBGAKLEKANAAYKM 420  
Db 361 ESEBEDDGLPKKMPITVDASYGGRGVGIIKMEVWGEKSTEBGAKLEKANAAYKM 420  
Qy 421 PEOEYEPPEPRNLNNMRSPSPRKWSPYIKGKLDALVLLRKGYDRVSVMRPOGDTGR 480  
Db 421 PEOEYEPPEPRNLNNMRSPSPRKWSPYIKGKLDALVLLRKGYDRVSVMRPOGDTGR 480  
Qy 481 CINFRVKNQOPAKYPLNNAVHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSPSTL 540  
Db 481 CINFRVKNQOPAKYPLNNAVHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSPSTL 540  
Qy 541 PPPQAPPNNRAPPSPRPPPSV 564  
Db 541 PPPQAPPNNRAPPSPRPPPSV 564

## RESULT 2

US-09-918-715-232  
; Sequence 232, Application US/09918715  
; Publication No. US20030017157A1  
; GENERAL INFORMATION:  
; APPLICANT: Brad St. Croix  
; APPLICANT: Bert Vogelstein  
; APPLICANT: Kenneth Kinzler  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00134  
; CURRENT FILING DATE: 2001-08-01  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 232  
; LENGTH: 564  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-918-715-232

Query Match 100.0%; Score 3025; DB 12; Length 564;  
Best Local Similarity 100.0%; Pred. No. 3,7e-225;  
Matches 564; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATARRALGIGFQWLSLTLVLTICAGGGRREDGACGFPDYFTLDKSGSVLHHMN 60  
Db 1 MATARRALGIGFQWLSLTLVLTICAGGGRREDGACGFPDYFTLDKSGSVLHHMN 60  
Qy 61 EIIYFVEQLAHKFTSPQLRMSFIVSTRTTLMKLTEDRQIRQGLELOKVLPGSDTYM 120  
Db 61 EIIYFVEQLAHKFTSPQLRMSFIVSTRTTLMKLTEDRQIRQGLELOKVLPGSDTYM 120  
Qy 121 HEGFERASEQIYYENRQGYRTASVIALITDGLHEDLFPYSERANRSDIGAIVYCVG 180  
Db 121 HEGFERASEQIYYENRQGYRTASVIALITDGLHEDLFPYSERANRSDIGAIVYCVG 180

Db 121 HEGFERASEQIYYENRQGYRTASVIALITDGLHEDLFPYSERANRSDIGAIVYCVG 180  
Qy 181 KDFNETOLARIADSKDHFVFNVDGFOALOGIISHILKSCIEILAAEPSTICAGESFOV 240  
Db 181 KDFNETOLARIADSKDHFVFNVDGFOALOGIISHILKSCIEILAAEPSTICAGESFOV 240  
Qy 241 VRNGGFHARNVDRVLCSPKINDSVTLNEKPFVSDTYLLCPAPILKEVGKALQVSMN 300  
Db 241 VRNGGFHARNVDRVLCSPKINDSVTLNEKPFVSDTYLLCPAPILKEVGKALQVSMN 300  
Qy 301 DGLSFSSSVIITTHCSDSIIAIALIIFLLAIALMLWFWPLCCTVIIKEVPPPAE 360  
Db 301 DGLSFSSSVIITTHCSDSIIAIALIIFLLAIALMLWFWPLCCTVIIKEVPPPAE 360  
Qy 361 ESEBEDDGLPKKMPITVDASYGGRGVGIIKMEVWGEKSTEBGAKLEKANAAYKM 420  
Db 361 ESEBEDDGLPKKMPITVDASYGGRGVGIIKMEVWGEKSTEBGAKLEKANAAYKM 420  
Qy 421 PEOEYEPPEPRNLNNMRSPSPRKWSPYIKGKLDALVLLRKGYDRVSVMRPOGDTGR 480  
Db 421 PEOEYEPPEPRNLNNMRSPSPRKWSPYIKGKLDALVLLRKGYDRVSVMRPOGDTGR 480  
Qy 481 CINFRVKNQOPAKYPLNNAVHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSPSTL 540  
Db 481 CINFRVKNQOPAKYPLNNAVHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSPSTL 540  
Qy 541 PPPQAPPNNRAPPSPRPPPSV 564  
Db 541 PPPQAPPNNRAPPSPRPPPSV 564

## RESULT 3

US-10-301-822-199  
; Sequence 199, Application US/10301822  
; Publication No. US20030148410A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Berger, Allison  
; APPLICANT: Guillemette, Tracy L.  
; APPLICANT: Kametkar, Shubhangi  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Monahan, John E.  
; APPLICANT: Thibodeau, Stephen N.  
; APPLICANT: Burgart, Lawrence J.  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; TITLE OF INVENTION: THERAPY OF COLON CANCER  
; FILE REFERENCE: MPM01-029P2RNM  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR FILING DATE: 2001-12-10  
; PRIOR FILING DATE: 2001-12-10  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR FILING DATE: 2002-05-20  
; NUMBER OF SEQ ID NOS: 228  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 199  
; LENGTH: 564  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-301-822-199

Query Match 100.0%; Score 3025; DB 14; Length 564;  
Best Local Similarity 100.0%; Pred. No. 3,7e-225;  
Matches 564; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATARRALGIGFQWLSLTLVLTICAGGGRREDGACGFPDYFTLDKSGSVLHHMN 60  
Db 1 MATARRALGIGFQWLSLTLVLTICAGGGRREDGACGFPDYFTLDKSGSVLHHMN 60  
Qy 61 EIIYFVEQLAHKFTSPQLRMSFIVSTRTTLMKLTEDRQIRQGLELOKVLPGSDTYM 120  
Db 61 EIIYFVEQLAHKFTSPQLRMSFIVSTRTTLMKLTEDRQIRQGLELOKVLPGSDTYM 120



```

Db      ||| 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFYFSERANRSRDGAIVYCVG 180
Qy      ||| 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFYFSERANRSRDGAIVYCVG 180
Db      ||| 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFYFSERANRSRDGAIVYCVG 180
Qy      ||| 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIIHSLILKSCIEIIAABSTICAGSPFV 240
Db      ||| 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIIHSLILKSCIEIIAABSTICAGSPFV 240
Qy      ||| 241 VRGNGFRHARNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300
Db      ||| 241 VRGNGFRHARNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300
Qy      ||| 301 DGLSFISSSVITTTTHCSGDSIIALILFLALALMLMFWPLCTCVIIKEVPPPAE 360
Db      ||| 301 DGLSFISSSVITTTTHCSGDSIIALILFLALALMLMFWPLCTCVIIKEVPPPAE 360
Qy      ||| 361 ESEEDDDGLPKKKMPTVDASYGGRGVGIIKMEVNRGEKSTEGAKLEKAKARVYM 420
Db      ||| 361 ESEEDDDGLPKKKMPTVDASYGGRGVGIIKMEVNRGEKSTEGAKLEKAKARVYM 420
Qy      ||| 421 PEOEYEPERPNLNNMRSPSSPRKWSPIKGLDALWVLLRKGDRYSVMRPOGDTGR 480
Db      ||| 421 PEOEYEPERPNLNNMRSPSSPRKWSPIKGLDALWVLLRKGDRYSVMRPOGDTGR 480
Qy      ||| 481 CINFTRVKNOPAKYPLNNAVHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSBSTL 540
Db      ||| 481 CINFTRVKNOPAKYPLNNAVHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSBSTL 540
Qy      ||| 541 PPPQAPPNNRAPPSRPPRPSV 564
Db      ||| 541 PPPQAPPNNRAPPSRPPRPSV 564

```

## RESULT 4

```

US-10-408-765A-1823
; Sequence 1823, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boia D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408.765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1823
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1823

```

```

Query Match      100.0%; Score 3025; DB 16; Length 564;
Best Local Similarity 100.0%; Pred. No. 3.7e-225;
Matches 564; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 NATAERBALGIGFOWLSLATLVICAGCGRRDDGPACYGFDLYFIIDKSGSVLHNN 60
Db      1 NATAERBALGIGFOWLSLATLVICAGCGRRDDGPACYGFDLYFIIDKSGSVLHNN 60
Qy      61 EIIYVEEQIAHKFISPOLMSFIVSTRGTTLMLKLTEDREQIRQGLEIOLKVLPGSDTYM 120
Db      61 EIIYVEEQIAHKFISPOLMSFIVSTRGTTLMLKLTEDREQIRQGLEIOLKVLPGSDTYM 120

```

```

Qy      ||| 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFYFSERANRSRDGAIVYCVG 180
Db      ||| 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFYFSERANRSRDGAIVYCVG 180
Qy      ||| 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIIHSLILKSCIEIIAABSTICAGSPFV 240
Db      ||| 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIIHSLILKSCIEIIAABSTICAGSPFV 240
Qy      ||| 241 VRGNGFRHARNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300
Db      ||| 241 VRGNGFRHARNDVLCSEFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300
Qy      ||| 301 DGLSFISSSVITTTTHCSGDSIIALILFLALALMLMFWPLCTCVIIKEVPPPAE 360
Db      ||| 301 DGLSFISSSVITTTTHCSGDSIIALILFLALALMLMFWPLCTCVIIKEVPPPAE 360
Qy      ||| 361 ESEEDDDGLPKKKMPTVDASYGGRGVGIIKMEVNRGEKSTEGAKLEKAKARVYM 420
Db      ||| 361 ESEEDDDGLPKKKMPTVDASYGGRGVGIIKMEVNRGEKSTEGAKLEKAKARVYM 420
Qy      ||| 421 PEOEYEPERPNLNNMRSPSSPRKWSPIKGLDALWVLLRKGDRYSVMRPOGDTGR 480
Db      ||| 421 PEOEYEPERPNLNNMRSPSSPRKWSPIKGLDALWVLLRKGDRYSVMRPOGDTGR 480
Qy      ||| 481 CINFTRVKNOPAKYPLNNAVHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSBSTL 540
Db      ||| 481 CINFTRVKNOPAKYPLNNAVHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSBSTL 540
Qy      ||| 541 PPPQAPPNNRAPPSRPPRPSV 564
Db      ||| 541 PPPQAPPNNRAPPSRPPRPSV 564

```

## RESULT 5

```

US-09-918-715-194
; Sequence 194, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918.715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 194
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-918-715-194

```

```

Query Match      95.9%; Score 2901; DB 12; Length 562;
Best Local Similarity 96.8%; Pred. No. 1.4e-215;
Matches 538; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
Qy      9 LGIGFOWLSLATLVICAGCGRRDDGPACYGFDLYFIIDKSGSVLHNNIYFVEQ 68
Db      7 LGAGRGICVAALVIVCAGHGRREDGPACYGFDLYFIIDKSGSVLHNNIYFVEQ 66
Qy      69 LAHRTISPOLMSFIVSTRGTTLMLKLTEDREQIRQGLEIOLKVLPGSDTYMHSEFERAS 128
Db      67 LAHRTISPOLMSFIVSTRGTTLMLKLTEDREQIRQGLEIOLKVLPGSDTYMHSEFERAS 126
Qy      129 EOIYENRQGYRTASVIALTDGELHEDLFYFSERANRSRDGAIVYCVGKDFNETOL 188

```

Db 127 EQIYVENSQGYRTASVITLALTDGELHEDLFFYSEREANRSDLGAIYVGVGKDFNETOL 186  
Qy 189 ARIADSKDHVPVNDGFQALOGIHSILKKSCEIILAEPSSTICAGESFOVVVWNGNGFRH 248  
Db 187 ARIADSKDHVPVNDGFQALOGIHSILKKSCEIILAEPSSTICAGESFOVVVWNGNGFRH 246  
Qy 249 ARNDRVLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKAAQVSNNDGLSFTSS 308  
Db 247 ARNDRVLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKAAQVSNNDGLSFTSS 306  
Qy 309 SVITTTTCHSDGSLIALALVFLFLALALLMFMPLCCTVIIEVPPPAEESSEBDD 368  
Db 307 SVITTTTCHSDGSLIALALVFLFLALALLMFMPLCCTVIIEVPPPAEESSEBDD 366  
Qy 369 GLPKKKMPTVDASYGGRGVGGIKRMEVRWGEKSTEGALKLEKAKNARVMPQEYFEP 428  
Db 367 GLPKKKMPTVDASYGGRGVGGIKRMEVRWGEKSTEGALKLEKAKNARVMPQEYFEP 426  
Qy 429 EPRNLNNMRRPSSPRKWSPIKGLDALVWLRLKGYDRVSVMRPOGDTGRCINFTRVK 488  
Db 427 EPRNLNNMRRPSSPRKWSPIKGLDALVWLRLKGYDRVSVMRPOGDTGRCINFTRVK 486  
Qy 489 NNOPAKYPLNNAHYTSSPPAPITYTTPPPAPHCPPPPSAFTPTPIPSPTLPPPPQAPP 548  
Db 487 NSOPAKYPLNNTYHSSPPAPITYTTPPPAPHCPPPPSAFTPTPIPSPTLPPPPQAPP 546  
Qy 549 PNRAAPPSPRPPPSV 564  
Db 547 PNRAAPPSPRPPPSV 562

RESULT 6  
US-09-918-715-301  
; Sequence 301, Application US/09918715  
; Publication No. US20030017157A1  
; GENERAL INFORMATION:  
; APPLICANT: Brad St. Croix  
; APPLICANT: Bert Vogelstein  
; APPLICANT: Kenneth Kinzler  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00134  
; CURRENT APPLICATION NUMBER: US/09/918,715  
; PRIOR FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/222,599  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR APPLICATION NUMBER: 60/224,360  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/282,850  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 301  
; LENGTH: 562  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-918-715-301

Query Match 95.9% Score 2901; DB 12: Length 562;  
Best Local Similarity 96.8% Pred. No. 1.4e-215;  
Matches 538; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Qy 9 LGIGFQWLSLTVLVCAGGGRREDGGPACYGFDLYFLDKSGSVLHNNNEIYYFEQ 68  
Db 7 LGAGRGCAVALVVCAGHGRREDGGPACYGFDLYFLDKSGSVLHNNNEIYYFEQ 66  
Qy 69 LAHFISQOLMSFVSTRTGTTLMKLTEDRBOIRQGLEBIQVLPGGDTYMHGFERAS 128  
Db 67 LAHFISQOLMSFVSTRTGTTLMKLTEDRBOIRQGLEBIQVLPGGDTYMHGFERAS 126  
Qy 129 EQIYVENSQGYRTASVITLALTDGELHEDLFFYSEREANRSDLGAIYVGVGKDFNETOL 188  
Db 127 EQIYVENSQGYRTASVITLALTDGELHEDLFFYSEREANRSDLGAIYVGVGKDFNETOL 186

Qy 189 ARIADSKDHVPVNDGFQALOGIHSILKKSCEIILAEPSSTICAGESFOVVVWNGNGFRH 248  
Db 187 ARIADSKDHVPVNDGFQALOGIHSILKKSCEIILAEPSSTICAGESFOVVVWNGNGFRH 246  
Qy 249 ARNDRVLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKAAQVSNNDGLSFTSS 308  
Db 247 ARNDRVLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGMKAAQVSNNDGLSFTSS 306  
Qy 309 SVITTTTCHSDGSLIALALVFLFLALALLMFMPLCCTVIIEVPPPAEESSEBDD 368  
Db 307 SVITTTTCHSDGSLIALALVFLFLALALLMFMPLCCTVIIEVPPPAEESSEBDD 366  
Qy 369 GLPKKKMPTVDASYGGRGVGGIKRMEVRWGEKSTEGALKLEKAKNARVMPQEYFEP 428  
Db 367 GLPKKKMPTVDASYGGRGVGGIKRMEVRWGEKSTEGALKLEKAKNARVMPQEYFEP 426  
Qy 429 EPRNLNNMRRPSSPRKWSPIKGLDALVWLRLKGYDRVSVMRPOGDTGRCINFTRVK 488  
Db 427 EPRNLNNMRRPSSPRKWSPIKGLDALVWLRLKGYDRVSVMRPOGDTGRCINFTRVK 486  
Qy 489 NNOPAKYPLNNAHYTSSPPAPITYTTPPPAPHCPPPPSAFTPTPIPSPTLPPPPQAPP 548  
Db 487 NSOPAKYPLNNTYHSSPPAPITYTTPPPAPHCPPPPSAFTPTPIPSPTLPPPPQAPP 546  
Qy 549 PNRAAPPSPRPPPSV 564  
Db 547 PNRAAPPSPRPPPSV 562

RESULT 7  
US-09-796-753-24  
; Sequence 24, Application US/09796753  
; Publication No. US20030027998A1  
; GENERAL INFORMATION:  
; APPLICANT: McCarthy, Sean A.  
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF  
; FILE REFERENCE: 7853-227-999  
; CURRENT APPLICATION NUMBER: US/09/796,753  
; PRIOR FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: 09/183,175  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: 09/223,094  
; PRIOR FILING DATE: 1998-12-30  
; PRIOR APPLICATION NUMBER: 09/223,546  
; PRIOR FILING DATE: 1998-12-30  
; PRIOR APPLICATION NUMBER: 09/224,246  
; PRIOR FILING DATE: 1998-12-30  
; PRIOR APPLICATION NUMBER: 09/259,388  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/122,458  
; PRIOR FILING DATE: 1999-03-01  
; PRIOR APPLICATION NUMBER: 09/312,359  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: 09/336,536  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: 09/342,687  
; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: 09/345,464  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: 09/365,164  
; PRIOR FILING DATE: 1999-07-30  
; PRIOR APPLICATION NUMBER: 09/399,723  
; PRIOR FILING DATE: 1999-09-20  
; PRIOR APPLICATION NUMBER: 09/409,634  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 09/471,179  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 09/474,071  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: 09/474,072  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: 09/514,010  
; PRIOR FILING DATE: 2000-02-25

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; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 24
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Mouse
US-09-796-753-24

```

Query Match 66.7%; Score 2017; DB 10; Length 381;

Best Local Similarity 98.1%; Pred. No. 1.9e-147; Indels 0; Gaps 0; Matches 371; Conservative 3; Mismatches 4;

```

QY 187 QIARIADSKDHFVPVNDGFOALOGIHSILKKSCEIIAABPSTICAGESFQVVRGNGF 246
DB 4 QIARIADSKDHFVPVNDGFOALOGIHSILKKSCEIIAABPSTICAGESFQVVRGNGF 63
QY 247 RHARVNDVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFI 306
DB 64 RHARVNDVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFI 123
QY 307 SSSVITTTTHCSDSIIAIIALLIFLLALALLMFWPFLCCTVITKEVPPPAEESBED 366
DB 124 SSSVITTTTHCSDSIIAIIALLIFLLALALLMFWPFLCCTVITKEVPPPAEESBED 183
QY 367 DDGLPKKKMPTVDASYGGRGVGGIKRMEVWGEKSTEBGAKLEKANNARVKMPEQYE 426
DB 184 DDGLPKKKMPTVDASYGGRGVGGIKRMEVWGEKSTEBGAKLEKANNARVKMPEQYE 243
QY 427 FPEPNLNMMNRSPSPKMWSPKIGKLDALMWLLRKGYDRVSVMRPOGDTGRGCIINFTR 486
DB 244 FPEPNLNMMNRSPSPKMWSPKIGKLDALMWLLRKGYDRVSVMRPOGDTGRGCIINFTR 303
QY 487 VKNNOPAKYPLNNAYHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSPTLPPPOA 546
DB 304 VKNNOPAKYPLNNAYHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSPTLPPPOA 363
QY 547 PPNRAPPSPRPPPSV 564
DB 364 PPNRAPPSPRPPPSV 381

```

```

RESULT 8
US-10-038-307-4
; Sequence 4, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0

```

```

; SEQ ID NO 4
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Murine
US-10-038-307-4

```

Query Match 66.7%; Score 2017; DB 14; Length 381;

Best Local Similarity 98.1%; Pred. No. 1.9e-147; Indels 0; Gaps 0; Matches 371; Conservative 3; Mismatches 4;

```

QY 187 QIARIADSKDHFVPVNDGFOALOGIHSILKKSCEIIAABPSTICAGESFQVVRGNGF 246
DB 4 QIARIADSKDHFVPVNDGFOALOGIHSILKKSCEIIAABPSTICAGESFQVVRGNGF 63
QY 247 RHARVNDVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFI 306
DB 64 RHARVNDVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFI 123
QY 307 SSSVITTTTHCSDSIIAIIALLIFLLALALLMFWPFLCCTVITKEVPPPAEESBED 366
DB 124 SSSVITTTTHCSDSIIAIIALLIFLLALALLMFWPFLCCTVITKEVPPPAEESBED 183
QY 367 DDGLPKKKMPTVDASYGGRGVGGIKRMEVWGEKSTEBGAKLEKANNARVKMPEQYE 426
DB 184 DDGLPKKKMPTVDASYGGRGVGGIKRMEVWGEKSTEBGAKLEKANNARVKMPEQYE 243
QY 427 FPEPNLNMMNRSPSPKMWSPKIGKLDALMWLLRKGYDRVSVMRPOGDTGRGCIINFTR 486
DB 244 FPEPNLNMMNRSPSPKMWSPKIGKLDALMWLLRKGYDRVSVMRPOGDTGRGCIINFTR 303
QY 487 VKNNOPAKYPLNNAYHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSPTLPPPOA 546
DB 304 VKNNOPAKYPLNNAYHTSSPPAPITYTPPPAPHCPPPPSAPTPIPSPTLPPPOA 363
QY 547 PPNRAPPSPRPPPSV 564
DB 364 PPNRAPPSPRPPPSV 381

```

#### RESULT 9

```

US-10-201-292-4
; Sequence 4, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Murine
US-10-201-292-4

```

Query Match 66.7%; Score 2017; DB 14; Length 381;

Best Local Similarity 98.1%; Pred. No. 1.9e-147; Indels 0; Gaps 0; Matches 371; Conservative 3; Mismatches 4;

```

QY 187 QIARIADSKDHFVPVNDGFOALOGIHSILKKSCEIIAABPSTICAGESFQVVRGNGF 246
DB 4 QIARIADSKDHFVPVNDGFOALOGIHSILKKSCEIIAABPSTICAGESFQVVRGNGF 63
QY 247 RHARVNDVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFI 306
DB 64 RHARVNDVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMNDGLSFI 123
QY 307 SSSVITTTTHCSDSIIAIIALLIFLLALALLMFWPFLCCTVITKEVPPPAEESBED 366

```

Db 124 SSSVITTTTHCSGDSIIAIALVLLFLALALMLWMFPLCCTVITKEVPPPESEBED 183  
Qy 367 DDGLPKKKWPTVDASYGGRGVGIGKMEVWGEKSTEEBAKLEKANAARVKEQOYE 426  
Db 184 DDGLPKKKWPTVDASYGGRGVGIGKMEVWGEKSTEEBAKLEKANAARVKEQOYE 243  
Qy 427 FPEPNLNMMNRPPSPKMYSPISIKGLDALVLLRKGYDRVSVVRPQPGDTGRCINFTR 486  
Db 244 FPEPNLNMMNRPPSPKMYSPISIKGLDALVLLRKGYDRVSVVRPQPGDTGRCINFTR 303  
Qy 487 VKNQAPARYPLNNAYHTSSPPAPITYTPPPAPHCPPPPSAPPPPIPSPTLPPPPQA 546  
Db 304 VKNQAPARYPLNNAYHTSSPPAPITYTPPPAPHCPPPPSAPPPPIPSPTLPPPPQA 363  
Qy 547 PPPNAPPPSPRRPPPSV 564  
Db 364 PPPNAPPPSPRRPPPSV 381

## RESULT 10

US-09-833-245-621  
; Sequence 621, Application US/09833245  
; Publication No. US20040010134A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Albumin Fusion Proteins  
; FILE REFERENCE: PFS46PCT  
; CURRENT APPLICATION NUMBER: US/09/833,245  
; CURRENT FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 60/229, 358  
; PRIOR FILING DATE: 2000-04-12  
; PRIOR APPLICATION NUMBER: 60/256, 931  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/199, 384  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 2267  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 621  
; LENGTH: 403  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-833-245-621

Query Match 62.6%; Score 1893.5; DB 11; Length 403;  
Best Local Similarity 94.8%; Pred. No. 7.1e-138;

Matches 367; Conservative 2; Mismatches 7; Indels 11; Gaps 1;

Qy 1 MATERRALGIGFQWLSLATTVLICAGQGRREDGPAICYGFDLYFTLDKSGSVLHHMN 60  
Db 1 MATERRALGIGFQWLSLATTVLICAGQGRREDGPAICYGFDLYFTLDKSGSVLHHMN 60  
Qy 61 EIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQIRQGLELOKVLPGDPTYM 120  
Db 61 EIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQIRQGLELOKVLPGDPTYM 120  
Qy 121 HEGFERASEQIYYENRQGYRTASVITIALTDGELHEDLFFYSERBRANSRDIGAIYVCV 180  
Db 121 HEGFERASEQIYYENRQGYRTASVITIALTDGELHEDLFFYSERBRANSRDIGAIYVCV 180  
Qy 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAABPSTICAGESFOV 240  
Db 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAABPSTICAGESFOV 240  
Qy 241 VRGNFRRHARNDVRLCSFKINDSVTLNEKPFVSEDYLLCPAPILKEVGKALQVSMN 300  
Db 241 VRGNFRRHARNDVRLCSFKINDSVTLNEKPFVSEDYLLCPAPILKEVGKALQVSMN 300  
Qy 301 DGLSFSSSVIITTHCSGDSIIAIALVLLFLALALMLWMFPLCCTVITKEVPPPAE 360  
Db 301 DGLSFSSSVIITTHCSGDSIIAIALVLLFLALALMLWMFPLCCTVITKEVPPPAE 360  
Qy 361 ESEBEDDGLPKKKWPTVDASYGGRG 387

Db 361 ESEVSDHSMRA-----VGGQG 376

## RESULT 11

US-09-833-245-620  
; Sequence 620, Application US/09833245  
; Publication No. US20040010134A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Albumin Fusion Proteins  
; FILE REFERENCE: PFS46PCT  
; CURRENT APPLICATION NUMBER: US/09/833,245  
; CURRENT FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 60/229, 358  
; PRIOR FILING DATE: 2000-04-12  
; PRIOR APPLICATION NUMBER: 60/256, 931  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/199, 384  
; NUMBER OF SEQ ID NOS: 2267  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 620  
; LENGTH: 403  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (175)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (320)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (331)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (368)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-833-245-620

Query Match 62.0%; Score 1874; DB 11; Length 403;  
Best Local Similarity 98.6%; Pred. No. 2.3e-136;

Matches 361; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MATERRALGIGFQWLSLATTVLICAGQGRREDGPAICYGFDLYFTLDKSGSVLHHMN 60  
Db 1 MATERRALGIGFQWLSLATTVLICAGQGRREDGPAICYGFDLYFTLDKSGSVLHHMN 60  
Qy 61 EIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQIRQGLELOKVLPGDPTYM 120  
Db 61 EIYFVEQLAHKFISPOLRMSFIVSTRGTTLMKLTEDREQIRQGLELOKVLPGDPTYM 120  
Qy 121 HEGFERASEQIYYENRQGYRTASVITIALTDGELHEDLFFYSERBRANSRDIGAIYVCV 180  
Db 121 HEGFERASEQIYYENRQGYRTASVITIALTDGELHEDLFFYSERBRANSRDIGAIYVCV 180  
Qy 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAABPSTICAGESFOV 240  
Db 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAABPSTICAGESFOV 240  
Qy 241 VRGNFRRHARNDVRLCSFKINDSVTLNEKPFVSEDYLLCPAPILKEVGKALQVSMN 300  
Db 241 VRGNFRRHARNDVRLCSFKINDSVTLNEKPFVSEDYLLCPAPILKEVGKALQVSMN 300  
Qy 301 DGLSFSSSVIITTHCSGDSIIAIALVLLFLALALMLWMFPLCCTVITKEVPPPAE 360  
Db 301 DGLSFSSSVIITTHCSGDSIIAIALVLLFLALALMLWMFPLCCTVITKEVPPPAE 360  
Qy 361 ESEBED 366  
Db 361 ESEVSD 366

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RESULT 12
US-10-038-307-18
/ Sequence 18, Application US/10038307
/ Publication No. US20030134786A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZKAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/038,307
/ CURRENT FILING DATE: 2002-06-28
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 18
/ LENGTH: 551
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-038-307-18

Query Match          54.9%; Score 1661; DB 14; Length 551;
Best Local Similarity 100.0%; Pred. No. 1e-119;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATARRALGIGFQWLSLTLVLIICAGGGRREDGGPACYGFDLYFLIDKSGSVLHNMN 60
DB 1 MATARRALGIGFQWLSLTLVLIICAGGGRREDGGPACYGFDLYFLIDKSGSVLHNMN 60
QY 61 EIVYVEQLAHKFIISPOLRMSFIVSTRTGTLMLTEREQRIRGLERLOKVLPGDPTM 120
DB 61 EIVYVEQLAHKFIISPOLRMSFIVSTRTGTLMLTEREQRIRGLERLOKVLPGDPTM 120
QY 121 HEGFERASEQIYYENRQGYRTASVIALTDGLHEDLFFYSERENRSDGAIYVCYGV 180
DB 121 HEGFERASEQIYYENRQGYRTASVIALTDGLHEDLFFYSERENRSDGAIYVCYGV 180
QY 181 KOPNETOLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIILAEPSTICAGSFPQV 240
DB 181 KOPNETOLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIILAEPSTICAGSFPQV 240
QY 241 VRGNGFRHARNDVRLCSFKINDSVTLNKEPFSVEDTYLLCPAPLKEVGKKAALQVSMN 300
DB 241 VRGNGFRHARNDVRLCSFKINDSVTLNKEPFSVEDTYLLCPAPLKEVGKKAALQVSMN 300
QY 301 DGLSFISSSVITTTTHCSDG 320
DB 301 DGLSFISSSVITTTTHCSDG 320

RESULT 13
US-10-201-292-18
/ Sequence 18, Application US/10201292
/ Publication No. US20030144193A1
/ GENERAL INFORMATION:
/ APPLICANT: James B. ROTTMAN
/ APPLICANT: Theresa L. O'KEEFE
/ APPLICANT: Engin OZKAYNAK
/ APPLICANT: Judith J. HEALEY
/ TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
/ FILE REFERENCE: 7853-253-999
/ CURRENT APPLICATION NUMBER: US/10/201,292
/ CURRENT FILING DATE: 2003-02-14
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 18
/ LENGTH: 551
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-201-292-18

Query Match          54.9%; Score 1661; DB 14; Length 551;
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Best Local Similarity 100.0%; Pred. No. 1e-119;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATARRALGIGFQWLSLTLVLIICAGGGRREDGGPACYGFDLYFLIDKSGSVLHNMN 60
DB 1 MATARRALGIGFQWLSLTLVLIICAGGGRREDGGPACYGFDLYFLIDKSGSVLHNMN 60
QY 61 EIVYVEQLAHKFIISPOLRMSFIVSTRTGTLMLTEREQRIRGLERLOKVLPGDPTM 120
DB 61 EIVYVEQLAHKFIISPOLRMSFIVSTRTGTLMLTEREQRIRGLERLOKVLPGDPTM 120
QY 121 HEGFERASEQIYYENRQGYRTASVIALTDGLHEDLFFYSERENRSDGAIYVCYGV 180
DB 121 HEGFERASEQIYYENRQGYRTASVIALTDGLHEDLFFYSERENRSDGAIYVCYGV 180
QY 181 KOPNETOLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIILAEPSTICAGSFPQV 240
DB 181 KOPNETOLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIILAEPSTICAGSFPQV 240
QY 241 VRGNGFRHARNDVRLCSFKINDSVTLNKEPFSVEDTYLLCPAPLKEVGKKAALQVSMN 300
DB 241 VRGNGFRHARNDVRLCSFKINDSVTLNKEPFSVEDTYLLCPAPLKEVGKKAALQVSMN 300
QY 301 DGLSFISSSVITTTTHCSDG 320
DB 301 DGLSFISSSVITTTTHCSDG 320

RESULT 14
US-09-796-753-12
/ Sequence 12, Application US/09796753
/ Publication No. US20030027998A1
/ GENERAL INFORMATION:
/ APPLICANT: McCarthy, Sean A.
/ TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
/ FILE REFERENCE: 7853-227-999
/ CURRENT APPLICATION NUMBER: US/09/796,753
/ CURRENT FILING DATE: 2001-03-01
/ PRIOR APPLICATION NUMBER: 09/183,175
/ PRIOR FILING DATE: 1998-10-30
/ PRIOR APPLICATION NUMBER: 09/223,094
/ PRIOR FILING DATE: 1998-12-30
/ PRIOR APPLICATION NUMBER: 09/223,546
/ PRIOR FILING DATE: 1998-12-30
/ PRIOR APPLICATION NUMBER: 09/224,246
/ PRIOR FILING DATE: 1998-12-30
/ PRIOR APPLICATION NUMBER: 09/259,388
/ PRIOR FILING DATE: 1999-02-26
/ PRIOR APPLICATION NUMBER: 60/1122,458
/ PRIOR FILING DATE: 1999-03-01
/ PRIOR APPLICATION NUMBER: 09/312,359
/ PRIOR FILING DATE: 1999-05-14
/ PRIOR APPLICATION NUMBER: 09/336,536
/ PRIOR FILING DATE: 1999-06-18
/ PRIOR APPLICATION NUMBER: 09/342,687
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: 09/345,464
/ PRIOR FILING DATE: 1999-06-30
/ PRIOR APPLICATION NUMBER: 09/365,164
/ PRIOR FILING DATE: 1999-07-30
/ PRIOR APPLICATION NUMBER: 09/399,723
/ PRIOR FILING DATE: 1999-09-20
/ PRIOR APPLICATION NUMBER: 09/409,634
/ PRIOR FILING DATE: 1999-09-30
/ PRIOR APPLICATION NUMBER: 09/471,179
/ PRIOR FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: 09/474,071
/ PRIOR FILING DATE: 1999-12-29
/ PRIOR APPLICATION NUMBER: 09/474,072
/ PRIOR FILING DATE: 1999-12-29
/ PRIOR APPLICATION NUMBER: 09/514,010
/ PRIOR FILING DATE: 2000-02-25
/ PRIOR APPLICATION NUMBER: 09/516,745
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; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: 09/572,002  
; PRIOR FILING DATE: 2000-05-14  
; PRIOR APPLICATION NUMBER: 09/597,993  
; PRIOR FILING DATE: 2000-06-19  
; PRIOR APPLICATION NUMBER: 09/599,596  
; PRIOR FILING DATE: 2000-06-22  
; PRIOR APPLICATION NUMBER: 09/630,334  
; PRIOR FILING DATE: 2000-07-31  
; PRIOR APPLICATION NUMBER: 09/606,565  
; PRIOR FILING DATE: 2000-06-29  
; PRIOR APPLICATION NUMBER: 09/606,317  
; PRIOR FILING DATE: 2000-06-29  
; PRIOR APPLICATION NUMBER: 09/665,666  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: 09/677,751  
; PRIOR FILING DATE: 2000-09-30  
; NUMBER OF SEQ ID NOS: 162  
; SEQ ID NO 12  
; LENGTH: 333  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-796-753-12

Query Match 54.5%; Score 1649; DB 10; Length 333;  
Best Local Similarity 100.0%; Pred. No. 4,4e-119;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATERRALGIGFOWLSATLVLCAGGGRREDGPGACYGFDLYFLIDKSGSVLHWN 60  
DB 1 MATERRALGIGFOWLSATLVLCAGGGRREDGPGACYGFDLYFLIDKSGSVLHWN 60  
QY 61 EIYFVEQLAHKFISPOLRMSFIVFSTRGTTLMKLTEDREOIRQGLBELQKVLPGSDTYM 120  
DB 61 EIYFVEQLAHKFISPOLRMSFIVFSTRGTTLMKLTEDREOIRQGLBELQKVLPGSDTYM 120  
QY 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSRDIGAIVYCVG 180  
DB 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSRDIGAIVYCVG 180  
QY 181 KDFNETQLARIADSKDHFVPVNDGFQALOGIISHILKSCIEILAEPSSTICAGESFQV 240  
DB 181 KDFNETQLARIADSKDHFVPVNDGFQALOGIISHILKSCIEILAEPSSTICAGESFQV 240  
QY 241 VRGNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKKAALQVSMN 300  
DB 241 VRGNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKKAALQVSMN 300  
QY 301 DGLSFSSSVIITTTTCS 318  
DB 301 DGLSFSSSVIITTTTCS 318

RESULT 15  
US-10-038-307-2  
; Sequence 2, Application US/10038307  
; Publication No. US20030134786A1  
; GENERAL INFORMATION:  
; APPLICANT: James B. ROTTMAN  
; APPLICANT: Theresa L. O'KEEFE  
; APPLICANT: Engin OZKAYNAK  
; APPLICANT: Judith J. HEALEY  
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
; FILE REFERENCE: 7853-253-999  
; CURRENT APPLICATION NUMBER: US/10/038,307  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 333  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-038-307-2

Query Match 54.5%; Score 1649; DB 14; Length 333;  
Best Local Similarity 100.0%; Pred. No. 4,4e-119;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATERRALGIGFOWLSATLVLCAGGGRREDGPGACYGFDLYFLIDKSGSVLHWN 60  
DB 1 MATERRALGIGFOWLSATLVLCAGGGRREDGPGACYGFDLYFLIDKSGSVLHWN 60  
QY 61 EIYFVEQLAHKFISPOLRMSFIVFSTRGTTLMKLTEDREOIRQGLBELQKVLPGSDTYM 120  
DB 61 EIYFVEQLAHKFISPOLRMSFIVFSTRGTTLMKLTEDREOIRQGLBELQKVLPGSDTYM 120  
QY 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSRDIGAIVYCVG 180  
DB 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSRDIGAIVYCVG 180  
QY 181 KDFNETQLARIADSKDHFVPVNDGFQALOGIISHILKSCIEILAEPSSTICAGESFQV 240  
DB 181 KDFNETQLARIADSKDHFVPVNDGFQALOGIISHILKSCIEILAEPSSTICAGESFQV 240  
QY 241 VRGNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKKAALQVSMN 300  
DB 241 VRGNGFRHARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKKAALQVSMN 300  
QY 301 DGLSFSSSVIITTTTCS 318  
DB 301 DGLSFSSSVIITTTTCS 318

Search completed: June 21, 2004, 14:02:13  
Job time : 57.2859 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 22, 2004, 02:37:46 ; Search time 548.154 Seconds

(without alignment)  
3075.489 Million cell updates/sec

Title: US-09-970-076-2

Perfect score: 1914  
Sequence: 1 MATERRALGIGFQWLSLAT.....VIEKVEPPPESESEKIK 368

## Scoring table:

BLOSUM62	Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Dgapop 6.0 , Dgapext 7.0	

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

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-O=/cgn2\_1/USPTO/US0970076/runac\_21062004\_125533\_8805/app\_query.fasta\_1.2140  
-DB=Published Applications NA -QPM=fastcap -SUFFIX=trpb -MINMATCH=0.1  
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40 cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=ppc -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US0970076\_@CNG\_1.1.1225\_@runac\_21062004\_125533\_8805  
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDP=6 -DELEXT=7

## Database : Published Applications NA:\*

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2:	/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6:	/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8:	/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9:	/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10:	/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14:	/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15:	/cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16:	/cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17:	/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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19:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
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1	1914	100.0	1454	16	US-10-133-937-58	Sequence 58, Appl
2	1914	100.0	1454	16	US-10-159-563-58	Sequence 58, Appl
3	1894	99.0	5540	13	US-09-918-715-176	Sequence 176, App
4	1894	99.0	5540	13	US-09-918-715-231	Sequence 231, App
5	1894	99.0	5540	15	US-10-301-822-198	Sequence 198, App
6	1793	93.7	5220	13	US-09-918-715-186	Sequence 186, App
7	1793	93.7	5220	13	US-09-918-715-300	Sequence 300, App
8	1661	86.8	1674	15	US-10-038-307-17	Sequence 17, Appl
9	1661	86.8	1674	15	US-10-201-292-17	Sequence 17, Appl
10	1650	86.2	1650	15	US-10-038-307-13	Sequence 13, Appl
11	1650	86.2	1650	15	US-10-038-307-15	Sequence 15, Appl
12	1650	86.2	1650	15	US-10-201-292-13	Sequence 13, Appl
13	1650	86.2	1650	15	US-10-201-292-15	Sequence 15, Appl
14	1649	86.2	1056	15	US-10-038-307-23	Sequence 23, Appl
15	1649	86.2	1056	15	US-10-201-292-23	Sequence 23, Appl
16	1649	86.2	1713	15	US-10-038-307-19	Sequence 19, Appl
17	1649	86.2	1713	15	US-10-201-292-19	Sequence 19, Appl
18	1649	86.2	2272	10	US-09-796-753-11	Sequence 11, Appl
19	1649	86.2	2272	15	US-10-038-307-1	Sequence 1, Appl
20	1649	86.2	2272	15	US-10-201-292-1	Sequence 1, Appl
21	1649	86.2	2352	15	US-10-198-846-9957	Sequence 9957, Ap
22	1649	86.2	2459	9	US-09-833-381-998	Sequence 998, App
23	1640	85.7	1650	15	US-10-038-307-9	Sequence 9, Appl
24	1640	85.7	1650	15	US-10-201-292-9	Sequence 9, Appl
25	1636	85.5	1008	15	US-10-038-307-25	Sequence 25, Appl
26	1636	85.5	1008	15	US-10-201-292-25	Sequence 25, Appl
27	1634.5	85.4	1047	15	US-10-038-307-21	Sequence 21, Appl
28	1634.5	85.4	1047	15	US-10-201-292-21	Sequence 21, Appl
29	1548	80.9	1608	15	US-10-201-292-15	Sequence 15, Appl
30	1520	79.4	2397	16	US-10-062-674-1757	Sequence 1757, Ap
31	1509	78.8	1623	15	US-10-038-307-11	Sequence 11, Appl
32	1509	78.8	1623	15	US-10-201-292-11	Sequence 11, Appl
33	1423	74.3	1534	15	US-10-201-292-33	Sequence 33, Appl
34	1392	72.7	1609	15	US-10-037-270-8	Sequence 8, Appl
35	1392	72.7	1609	16	US-10-117-222-8	Sequence 8, Appl
36	1313	62.6	1464	15	US-10-201-292-31	Sequence 31, Appl
37	1193	62.3	1401	15	US-10-201-292-27	Sequence 27, Appl
38	1193	62.3	1401	15	US-10-201-292-27	Sequence 27, Appl
39	962.5	50.3	2234	16	US-10-104-047-669	Sequence 669, App
40	962.5	50.3	4081	15	US-10-368-087-9	Sequence 9, Appl
41	957.5	50.0	3677	10	US-09-796-753-51	Sequence 51, Appl
42	957.5	50.0	3677	15	US-10-038-307-5	Sequence 5, Appl
43	957.5	50.0	3677	15	US-10-201-292-5	Sequence 5, Appl
44	957.5	50.0	4348	10	US-09-814-353-22000	Sequence 22000, A
45	941.5	49.2	5222	15	US-10-006-285-443	Sequence 443, App

## ALIGNMENTS

RESULT 1  
US-10-133-937-58  
; Sequence 58, Application US/10133937  
; Publication No. US20030207278A1  
GENERAL INFORMATION:  
APPLICANT: Khan, Javed  
APPLICANT: Ringner, Markus  
APPLICANT: Peterson, Carsten  
APPLICANT: Meltzer, Paul  
TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,  
TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND  
TITLE OF INVENTION: OTHER BIOLOGICAL STATES  
FILE REFERENCE: 11613.56US01  
CURRENT APPLICATION NUMBER: US/10/133,937  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 58  
LENGTH: 1454  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-133-937-58

## Alignment Scores:

Pred. No.: 5,086-239 Length: 1454  
 Score: 1914.00 Matches: 368  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 16 Gaps: 0

US-09-970-076-2 (1-368) x US-10-133-937-58 (1-1454)

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Oy 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
Db 144 ATGGCCAGCGGAGCGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTGGCCACT 203

Oy 21 LeuValLeuIleCyAlaGlyGlnGlyArgAlaGluArgAlaGlyProAlaCysTyr 40
Db 204 CTGGGCTCATCTGCGCGGCGAGGAGGAGCGAGGAGATGGGGGTCCAGCTGCTAC 263

Oy 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60
Db 264 GCGGATTTGACCTGTACTTCACTTTTGGACAATCAGAAAGTGTCTGCACACCTGGAAT 323

Oy 61 GluIleTyrTyrPheValGluGlnLeuAlaHisIleLysPheIleSerProGlnLeuArgMet 80
Db 324 GAAATCTATTACTTGTGGAAACAGTTGGCTCACAATAATCATCAGCCCAAGTTGAGATG 383

Oy 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
Db 384 TCCTTATTGTTTTCCTCCACCGAGAGAACACTTAAATGAACTGACAGAAAGACAGAA 443

Oy 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120
Db 444 CAAATCCGTCAGAGCCTTGAAGAACTCCAGAAAGTTGCCAGAGAGAGACACTTACATG 503

Oy 121 HisGluGlyPheGluArgAlaSerGlnGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140
Db 504 CATGAAGATTGTGAAGGGCCAGTGAAGATTATTTATGAAACAGCAAGAGGCTACAGG 563

Oy 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyr 160
Db 564 ACAGCCAGCGTCATATGCTTTCCTTGAAGTGAAGAACTCCAGAAAGTCTCTTTTCTAT 623

Oy 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
Db 624 TCAAGAGAGGAGGCTAATAGGCTCGAGATCTGGTGAATTTGTTTACGTGGTGGTGTG 683

Oy 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
Db 684 AAAAGTTTCAATGAGACACAGCTGGCCCGGATGGGACAGTAAAGATCATGTGTTTCCC 743

Oy 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220
Db 744 GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCTCAATTTTAAAGAAAGTCTGTC 803

Oy 221 IleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
Db 804 ATCGAAATTTAGCAGCTGAACATCAACCATATGTGCAGAGAGAGTCAATTTCAAGTGTG 863

Oy 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
Db 864 GTGAAGAGAAACGGCTTCCGACATGCCGCAACGAGGAGGAGGCTCTGCAAGCTTCAAG 923

Oy 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrThrLeuLeu 280
Db 924 ATCAATGACTCGGTACACTCAATAGAAAGCCCTTTCTGTGGAGAACTTATTTACTG 983

Oy 281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
Db 984 TGTCCAGGCGCATCTTAAAGAAAGTGGCATGAAGCTGCAGCTCAGAGTGAAC 1043

Oy 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
Db 1044 GATGGCTCTCTTTTATCTCCAGTTCTGTGATCATCAACACACACACACTGTTGTGACGGT 1103
  
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Oy 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTrp 340
Db 1104 TCCATCTGGCCATCGCCCTGCTGATCTGTCTCTGCTTCAAGCCCTGCTCTCTG 1163

Oy 341 TrpPheTrpProLeuCysCysThrValIleIleIleGluValProProProAlaGlu 360
Db 1164 TGGTTTGGCCCTCTGCTGACATGTATATCAAGAGAGGTCCCTCACCCCTGCCGAG 1223

Oy 361 GluSerGluGluLeuLysIleLys 368
Db 1224 GAGAGTAGAATAATAATAATAA 1247
  
```

## RESULT 2

US-10-159-563-58

; Sequence 58, Application US/10159563  
 ; Publication No. US2004009154A1  
 ; GENERAL INFORMATION:

; APPLICANT: Khan, Javed  
 ; APPLICANT: Ringner, Markus  
 ; APPLICANT: Peterson, Carsten

APPLICANT: Meltzer, Paul

TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR

FILE REFERENCE: 11613.56US11

CURRENT APPLICATION NUMBER: US/10/159,563

PRIOR FILING DATE: 2002-12-09

PRIOR APPLICATION NUMBER: US 10/133,937

NUMBER OF SEQ ID NOS: 444

SOFTWARE: PatentIn version 3.1

SEQ ID NO 58

LENGTH: 1454

TYPE: DNA

ORGANISM: Homo sapiens

US-10-159-563-58

## Alignment Scores:

Pred. No.: 5,086-239 Length: 1454  
 Score: 1914.00 Matches: 368  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 16 Gaps: 0

US-09-970-076-2 (1-368) x US-10-159-563-58 (1-1454)

```

Oy 1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
Db 144 ATGGCCAGCGGAGCGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTGGCCACT 203

Oy 21 LeuValLeuIleCyAlaGlyGlnGlyArgAlaGluArgAlaGlyProAlaCysTyr 40
Db 204 CTGGTGTCTATCTGCGCGGCGAAGGGGAGCGAGGAGAGATGGGGGTCCAGCTGCTAC 263

Oy 41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60
Db 264 GCGGATTTGACCTGTACTTTCCTCCACCGAGAGAACCTTAAATGAACTGACAGAAAGACAGAA 443

Oy 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
Db 384 TCCTTATTGTTTTCCTCCACCGAGAGAACCTTAAATGAACTGACAGAAAGACAGAA 443

Oy 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120
Db 444 CAAATCCGTCAGAGCCTTGAAGAACTCCAGAAAGTTGCCAGAGAGAGACACTTACATG 503

Oy 121 HisGluGlyPheGluArgAlaSerGlnGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140
  
```



```

Db      504 CATGAGGATTTGAAAGGGCCAGTAGAGATTATATGAAAAACAGCAAGAGGTACAGG 563
Qy      141 ThrAlaSerValIleIleAlaLeuThraSpGlyGluLeuHisGluAspLeuPhePheTyr 160
Db      564 ACAGCCACCGTCATATGCTTGTGACTGATGAGAACTCCATGAAATCTCTTTTTCAT 623
Qy      161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCyValGlyVal 180
Db      624 TCAGAGAGGAGGCTAAATGATGCTCGAATCTTGGTCAATTTGTTTACTGTTGTTGTTG 683
Qy      181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
Db      684 AAAGATTTCAATGAGACACAGCTGGCCCGGATGGGAGACATGAGATCATGTGTTTCCC 743
Qy      201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220
Db      744 GTGAATGACGGCTTTCAGGCTCTGCAGGACATCACTCAATTTTGAAGAAAGTCTGCG 803
Qy      221 IleguileuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
Db      804 ATCGAAATTTTAGCAGCTGACCATTCACATATGTCAGAGAGTCAATTCAGATGTC 863
Qy      241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
Db      864 GTGAGAGGAAACGGCTTCGACATGCCCGCAACGTGACAGGCTCTCTGACAGTTCAAG 923
Qy      261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrLeuLeu 280
Db      924 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGAGAGACACTAATTTTAC 983
Qy      281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
Db      984 TGTCACGCGCTATCTTAAAGAGTGGCATGAAAGCTGCACTCAGTCCAGTCCAGTGAAC 1043
Qy      301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSerAspGly 320
Db      1044 GATGCCCTCTCTTTATCTCCAGTCTGTGCATCATCAACACACACAGTGTCTGACCGT 1103
Qy      321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuLeuAlaLeuLeuTyr 340
Db      1104 TCCATCTGCGCCATGCGCTGCTGATCCGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1163
Qy      341 ThrPheTrpProLeuCysCysThrValIleIleLeuGlnValProProProProAlaGlu 360
Db      1164 TGGTCTGCGCCCTCTGCTGCACTGTGATTCAGAGAGTCCCTCCACCCCTGCGAG 1223
Qy      361 GluSerGluGluAsnLysIleLys 368
Db      1224 GAGACTGAGGAAATTAATAATAA 1247

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/ ORGANISM: Homo sapiens
US-09-918-715-176

Alignment Scores:
Pred. No.: 2e-235
Score: 1894.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 98.96%
DB: 13
Gaps: 0

US-09-970-076-2 (1-368) x US-09-918-715-176 (1-5540)

Qy      1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerIleuAlaThr 20
Db      144 ATGGCCACGGGAGAGGAGGAGCCCTCGGCATCGGCTTCAGTGGCTCTTTGGCCACT 203
Qy      21 LeuValLeuIleCysAlaGlyGlnGlyGlyArgArgGluAspGlyGlyProAlaCysTyr 40
Db      204 CTGGTGCATCTGGCCGGGCAAGGGGAGGAGGAGGAGATGGGGGTCCAGCCCTGTAC 263
Qy      41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTrpAsn 60
Db      264 GCGGATTTGACCTGTACTTCAATTTGGACAATCAGAGAGTGTGCTCACCACCTGGAAT 323
Qy      61 GluIleTyrTrpPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
Db      324 GAAATCTATTACTTTGTGAAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAGAAATG 383
Qy      81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
Db      384 TCTTTATGTTTCTTCCACCGAGAACCTTAAGAACTGAACAGAGACAGAGAA 443
Qy      101 GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120
Db      444 CAAATCCGTCAGGCGCTGAGAAAGCTCCAGAAAGTTCTGCAGAGAGACACTTACATG 503
Qy      121 HisGluGlyPheGluArgAlaSerGlnGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140
Db      504 CATGAGGATTTGAAAGGGCCAGTGAAGCATTTATTAAGAAACAGCAAGGGTACAGG 563
Qy      141 ThrAlaSerValIleIleAlaLeuThraSpGlyGluLeuHisGluAspLeuPhePheTyr 160
Db      564 ACAGCCACCGTCATATGCTTGTGACTGATGAGAACTCCATGAAAGTCTCTTTTCAT 623
Qy      161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCyValGlyVal 180
Db      624 TCAGAGAGGAGGCTAAATGATGCTCGAATCTTGGTCAATTTGTTTACTGTTGTTGTTG 683
Qy      181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
Db      684 AAAGATTTCAATGAGACACAGCTGGCCCGATGGGACAGTGAAGATCATGTGTTTCCC 743
Qy      201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220
Db      744 GTGAATGACGGCTTTCAGGCTCTGCAGGACATCACTCAATTTTGAAGAAAGTCTGCG 803
Qy      221 IleguileuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
Db      804 ATCGAAATTTTAGCAGCTGACCATTCACATATGTCAGAGAGTCAATTCAGATGTC 863
Qy      241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
Db      864 GTGAGAGGAAACGGCTTCGACATGCCCGCAACGTGACAGGCTCTCTGACAGTTCAAG 923
Qy      261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTyrLeuLeu 280
Db      924 ATCAATGACTCGGTCACTCAATGAGAAAGCCCTTTCTGTGAGAGATCAATTTTACTG 983
Qy      281 CysProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
Db      984 TGTCACGCGCTATCTTAAAGAGTGGCATGAAAGCTGCACTCAGTCCAGTCCAGTGAAC 1043

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Qy 301 AspglyLeuSerPheIleSerSerValIleIleIleThrThrHisCySeSerAspGly 320  
Db 1044 GATGGCCCTCTTTTATCTCCAGTTCTGTCATCATCACCAACACACTGTTTGGAGCGT 1103  
Qy 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTrp 340  
Db 1104 TCCATCCGGGCGCATCGCCCTCTGATCTGTTCCGCTCCAGCCCTGGCTCTCTCGG 1163  
Qy 341 TrpPheTrpProLeuCySeCySerThrValIleIleIleValIleProProProProAlaGlu 360  
Db 1164 TGGTTTCGCCCCCTCTGCTGCACTGTGATTATCAAGAGGTCCTCCACCCCTGCCGAG 1223  
Qy 361 GluSerGluGlu 364  
Db 1224 GAGAGTGAGAA 1235

RESULT 4  
US-09-918-715-231  
Sequence 231, Application US/09918715  
Publication No. US20030017157A1  
GENERAL INFORMATION:  
APPLICANT: Brad St. Croix  
APPLICANT: Bert Vogelstein  
APPLICANT: Kenneth Kinzler  
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
FILE REFERENCE: 1107.00134  
CURRENT APPLICATION NUMBER: US/09/918,715  
PRIORITY FILING DATE: 2001-08-01  
PRIORITY FILING DATE: 2000-08-02  
PRIORITY FILING DATE: 2000-08-02  
PRIORITY FILING DATE: 2000-08-11  
PRIORITY FILING DATE: 2000-08-11  
PRIORITY FILING DATE: 2000-04-11  
NUMBER OF SEQ ID NOS: 358  
SOFTWARE: FASTSEQ For Windows Version 3.0  
SEQ ID NO: 231  
LENGTH: 5540  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-918-715-231

Alignment Scores:  
Pred. No.: 2e-235 Length: 5540  
Score: 1894.00 Matches: 364  
Percent Similarity: 100.00% Conservatve: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.96% Indels: 0  
Gaps: 0

US-09-970-076-2 (1-368) x US-09-918-715-231 (1-5540)

Qy 1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20  
Db 144 ATGGCCAGGGCGGAGGAGAGCCCTCGGCATCGGCTTCACAGTGTCTCTTTGGCCACT 203  
Qy 21 LeuValIleuIleCySeAlaGlyGlnGlyIleArgArgGluAspGlyGlyProAlaCySerTrp 40  
Db 204 CTGGGCTCATCTGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 263  
Qy 41 GlyGlyPheAspLeuTrpPheIleLeuAlaPheIleSerGlySerValLeuHisIleTrpAsn 60  
Db 264 GCGCGATTTGACCTGTACTTCTTTGGACAAATCAGAGAGTGTCGACACACCTGGAAAT 323  
Qy 61 GluIleTrpTrpPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMet 80  
Db 324 GAAATCTATTACTTTGTGGAACAAGTGGCTCAAAATTCATCAGCCCAAGTTGAGAAATG 383  
Qy 81 SerPheIleValIlePheSerThrArgGlyThrThrIleuMetIleLeuThrGluAspArgGlu 100  
Db 384 TCCTTTATTGTTTCTTCCACCCGAGGAGAACCTTAAAGAACTGACAGAGAGAGAGAA 443  
Qy 101 GlnIleArgGlnGlyLeuGluGluLeuGlnIleValIleuProGlyGlyAspThrTrpMet 120

Db 444 CAATCCGTACAGGCTTAGAAGAACTCCAGAAAGTTCTGCCAGGAGAGACACTTACATG 503  
Qy 121 HisGluGlyPheGluArgAlaSerGluGlnIleTrpTrpGluAsnArgGlnGlyTrpArg 140  
Db 504 CATGAAGATTGTAAGAGGCGCAGTAGACAGATTATATGAAAAACAGACAAAGGATACAGG 563  
Qy 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisIleGluAspLeuPhePheTrp 160  
Db 564 ACAGCCAGCGTCATCATTTGCTTTGATGATGAGAGAACTCCATGAAAGATCTTTTTCAT 623  
Qy 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValIleTrpCySeValGlyVal 180  
Db 624 TCAGAGAGGAGGAGGCTAATAGTCTCGAGATCTTGCTCAATTGTTACTGTGTGGTGTG 683  
Qy 181 LysAspPheAsnGluTrpGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200  
Db 684 AAGATTTCATGTAGACACAGCTGCGCCGAGTTGCGACAGTAAGATCATGTGTTC 743  
Qy 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuValLysSerCySe 220  
Db 744 GTGAATGACCGCTTTCAAGGCTCTGCAAGGATCATCCACTCAATTTGAGAGAACTCTGCG 803  
Qy 221 IleGluIleLeuAlaIleGluProSerThrIleCySeAlaGlyGluSerPheGlnValVal 240  
Db 804 ATCGAAATTCAGACGCTGAACCATCCACATATGTCCAGAGAGATTCATTCAAGTTGTC 863  
Qy 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCySeSerPheLys 260  
Db 864 GTGAGAGAAACGCTTCCAGCATGCCGCAACCTGACAGAGGTCCTTGCAAGCTTCAG 923  
Qy 261 IleAsnAspSerValThrLeuAsnGluLysProPheSerValGluAspThrTrpLeuLeu 280  
Db 924 ATCAATGACTCGGCACACTCAATGAGAGCCCTTTCTGTGGAAGATCTTATTTCG 983  
Qy 281 CySeProAlaProIleLeuLysGluValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300  
Db 984 TGTCACGCGCTAATCTTAAAGAAAGTTGGCATGAACCTGCACCTCCAGGTCACGATGAC 1043  
Qy 301 AspglyLeuSerPheIleSerSerValIleIleIleThrThrHisCySeSerAspGly 320  
Db 1044 GATGGCCCTCTTTTATCTCCAGTTCTGTCATCATCACCAACACACTGTTTGGAGCGT 1103  
Qy 321 SerIleLeuAlaIleAlaLeuLeuIleLeuPheLeuLeuAlaLeuAlaLeuLeuTrp 340  
Db 1104 TCCATCCGGGCGCATCGCCCTCTGATCTGTTCCGCTCCAGCCCTGGCTCTCTCGG 1163  
Qy 341 TrpPheTrpProLeuCySeCySerThrValIleIleIleValIleProProProProAlaGlu 360  
Db 1164 TGGTTTCGCCCCCTCTGCTGCACTGTGATTATCAAGAGGTCCTCCACCCCTGCCGAG 1223  
Qy 361 GluSerGluGlu 364  
Db 1224 GAGAGTGAGAA 1235

RESULT 5  
US-10-301-822-198  
Sequence 198, Application US/10301822  
Publication No. US20030148410A1  
GENERAL INFORMATION:  
APPLICANT: Millennium Pharmaceuticals, Inc.  
APPLICANT: Berger, Allison  
APPLICANT: Guillemette, Tracy L.  
APPLICANT: Kamatkar, Shubhangi  
APPLICANT: Schlegel, Robert  
APPLICANT: Monahan, John E.  
APPLICANT: Thibodeau, Stephen N.  
APPLICANT: BURGART, Lawrence J.  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
TITLE OF INVENTION: THERAPY OF COLON CANCER  
FILE REFERENCE: MPM01-029P2RNM  
CURRENT APPLICATION NUMBER: US/10/301,822



Db 352 GGGGGCCCCCGAGAGATGGGGGACACAGCTTGCTACGAGAGATTCGACCTTACTTCATC 411  
 Oy LeuApLySerGlySerValLeuHsiHsITPANGluIleTyTyTyPheValGluGln 68  
 Db 412 CTGACAGATGACGAGAGATGTGCTGCACACCTGGAAATGAAATCTACTTCTGTGAGCAG 471  
 Oy LeuAlaHsiTyPheIleSerProGlnLeuArgMetSerPheIleValPheSerThrArg 88  
 Db 472 TTGGCTCATAGATTCATCAGCCCAAGCTAAGATGCTCTTCATGTTCTTCTTACTGCA 531  
 Oy GlyThrThrLeuMetLeuLeuThrGluAspArgGluGlnIleArgGlnGluLeuGlu 108  
 Db 532 GGGACAACTTTAAATGAACCTAACTGAGGACAGGAAACGATCCGACAGGCTTGAAAG 591  
 Oy LeuGlnValLeuProGlyGlyAspThrTyPheMetHsiGluGlyPheGluAspArg 128  
 Db 592 CTCGAGAAAGTTCTTCCAGAGAGACACTTACATGACGAGAGATTCGAGAGGCGCAGT 651  
 Oy GluGlnIleTyTyTyGluAspArgGlnGlyTyPheArgThrAlaSerValIleIleAlaLeu 148  
 Db 652 GAGCAGATTTACTATGAGAACAGTCAGAGATACAGAGCGGCGAGCTCATCGCGCTTG 711  
 Oy ThrAspGlyGluLeuHsiGluAspLeuPhePheTyPheSerGluArgGluAlaAspArgSer 168  
 Db 712 ACGGATGGGAGCTGCACAGAGACCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 771  
 Oy ArgAspLeuGlyAlaIleValTyTyTyValGlyValAspPheAspGluThrGlnLeu 188  
 Db 772 CGAGACTTGGTGGCTGTTTACTGCGCTTGGCGGTGAAAGATTCATGAAATCTCAGTTG 831  
 Oy AlaArgIleAlaAspSerLeuAspHsiValPheProValaAspArgGlyPheGlnAlaLeu 208  
 Db 832 GCTCGGATTGACAGACAGTAAGGACACGCTGTTCTCTGTAAGACAGGCTTCAGGCTCTC 891  
 Oy GlnGlyIleIleHsiSerIleLeuTyPheSerCysIleGluIleLeuAlaGluPro 228  
 Db 892 CAAGGCAATTATCTCACTCAATTTTAAAGAAATCTGCAATCGAAATCTGCGCGTGAACCA 951  
 Oy SerThrIleCysAlaGlyGluSerPheGlnValValaArgGlyAspGlyPheArgHsi 248  
 Db 952 TTCACCACTTGGCGGAGAGATCTTCAAGTGTGCTGTAAGAGAAATGCGCTTCGACAT 1011  
 Oy AlaArgAspValaAspArgValaLeuCysSerPheTyPheIleAspAspSerValThrLeuAsn 268  
 Db 1012 GCCCGCATGTGACAGAGGCTCTGCAAGCTTCAAAATCAATGACTGACGCTCAAT 1071  
 Oy GluTyPheProPheSerValGluAspThrTyPheLeuLeuCysProAlaProIleLeuGlu 288  
 Db 1072 GAGAGCCCTTGTGTAAGACACTTAATTTGCTGTGCCCAACCAATCTTGAAAGAA 1131  
 Oy ValGlyMetLeuValaIleGluGlnValaSerMetAspAspGlyLeuSerPheIleSerSer 308  
 Db 1132 GTTGGCAGTGAAGCTGCACCTGACAGTCAAGATGAACGAGGCTTCTTCTTCTTCCAGT 1191  
 Oy SerValIleIleThrThrThrIleCysSerAspGlySerIleLeuAlaIleAlaLeu 328  
 Db 1192 TCTGCATCATCACACACACACACTGTTCAAGCGGCTCATCTGCGATGCTGTGCTG 1251  
 Oy IleLeuPheLeuLeuLeuAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 348  
 Db 1252 GTCCCTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 1311  
 Oy ValIleIleTyGluValaProProProProAlaGluGluSerGluGlu 364  
 Db 1312 GTGATCATCAAGAGGCTCCCTCCACCCCTGTGAGAGAGTAGAGAA 1359

RESULT 7  
 US-09-918-715-300  
 ; Sequence 300, Application US/0918715  
 ; Publication No. US20030017157A1

; GENERAL INFORMATION:  
 ; APPLICANT: Brad St. Croix  
 ; APPLICANT: Bert Vogelstein

; APPLICANT: Kenneth Kinzler  
 ; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
 ; FILE REFERENCE: 1107.00134  
 ; CURRENT APPLICATION NUMBER: US/09/918, 715  
 ; CURRENT FILING DATE: 2001-08-01  
 ; PRIOR APPLICATION NUMBER: 60/222, 599  
 ; PRIOR FILING DATE: 2000-08-02  
 ; PRIOR APPLICATION NUMBER: 60/224,360  
 ; PRIOR FILING DATE: 2000-08-11  
 ; PRIOR APPLICATION NUMBER: 60/282,850  
 ; PRIOR FILING DATE: 2000-04-11  
 ; NUMBER OF SEQ ID NOS: 358  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 300  
 ; LENGTH: 5220  
 ; TYPE: DNA  
 ; ORGANISM: Mouse  
 ; US-09-918-715-300

## Alignment Scores:

Pred. No.:	2,83e-222	Length:	5220
Score:	1793.00	Matches:	342
Percent Similarity:	97.75%	Conservative:	6
Best Local Similarity:	96.07%	Mismatches:	8
Query Match:	93.68%	Indels:	0
DB:	13	Gaps:	0

US-09-970-076-2 (1-368) x US-09-918-715-300 (1-5220)

Oy 9 LeuGlyIleGlyPheGlnITPLeuSerLeuAlaThrLeuValLeuIleCysAlaGlyGln 28  
 Db 292 CTGGGTCGGGCGCTGCGGAGACTTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 351  
 Oy 29 GlyGlyArgArgGlyAspGlyGlyProAlaCysArgGlyGlyPheAspLeuTyPheIle 48  
 Db 352 GGGGGCCCGCGAG 411  
 Oy LeuAspLySerGlySerValLeuHsiHsITPANGluIleTyTyTyPheValGluGln 68  
 Db 412 CTGACAGATGACGAGAGATGTGCTGCACACCTGGAAATGAAATCTACTTCTGTGAGCAG 471  
 Oy LeuAlaHsiTyPheIleSerProGlnLeuArgMetSerPheIleValPheSerThrArg 88  
 Db 472 TTGGCTCATAGATTCATCAGCCCAAGCTAAGATGCTCTTCTTCTTCTTCTTCTTCTTCTG 531  
 Oy GlyThrThrLeuMetLeuLeuThrGluAspArgGluGlnIleArgGlnGluLeuGlu 108  
 Db 532 GGGACAACTTTAAATGAACCTAACTGAGGACAGGAAACGATCCGACAGGCTTGAAAG 591  
 Oy LeuGlnValLeuProGlyGlyAspThrTyPheMetHsiGluGlyPheGluAspArg 128  
 Db 592 CTCGAGAAAGTTCTTCCAGAGAGACACTTACATGACGAGAGATTCGAGAGGCGCAGT 651  
 Oy GluGlnIleTyTyTyGluAspArgGlnGlyTyPheArgThrAlaSerValIleIleAlaLeu 148  
 Db 652 GAGCAGATTTACTATGAGAACAGTCAGAGATACAGAGCGGCGAGCTCATGCTGCTG 711  
 Oy ThrAspGlyGluLeuHsiGluAspLeuPhePheTyPheSerGluArgGluAlaAspArgSer 168  
 Db 712 ACGGATGGGAGCTGCACAGAGACCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 771  
 Oy ArgAspLeuGlyAlaIleValTyTyTyValGlyValAspPheAspGluThrGlnLeu 188  
 Db 772 CGAGACTTGGTGGCTGTTTACTGCGCTTGGCGGTGAAAGATTCATGAAATCTCAGTTG 831  
 Oy AlaArgIleAlaAspSerLeuAspHsiValPheProValaAspArgGlyPheGlnAlaLeu 208  
 Db 832 GCTCGGATTGACAGACAGTAAGGACACGCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 891  
 Oy GlnGlyIleIleHsiSerIleLeuTyPheSerCysIleGluIleLeuAlaGluPro 228  
 Db 892 CAAGGCAATTATCTCACTCAATTTTAAAGAAATCTGCAATCGAAATCTGCGCGTGAACCA 951



Score:	1661.00	Matches:	320
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	86.78%	Indels:	0
DB:	15	Gaps:	0

US-09-970-076-2 (1-368) X US-10-201-292-17 (1-1674)

Oy	1	MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnIlePheLeuSerLeuAlaThr	20
Dp	13	ATGGCCACGGCGAGCGAGAGGCCCTTCGGCANTCGGCTTCCAGTGGCTCTTTGGCCACT	72
Oy	21	LeuValLeuIleCysAlaGlyGlnGlyIaArgArgIuaArgIyGlyProAlaCysTyr	40
Dp	73	CTGGTGTCTATCTGGCCCGGGCGAAGGGGAGCCAGAGAGAGATGGGGGTCAGCTGTCTAC	132
Oy	41	GlyGlyPheAspLeuTyrPheIleLeuAspIysSerGlySerValLeuHisIleTPAsn	60
Dp	133	GGGGGATTTGACCTGTACTTTCATTATTGGCAAAATCAGAAAGTGCTGCAACACTGGAAAT	192
Oy	61	GluIleTyrPhePheValGluGlnLeuAlaHisIleYsPheIleSerProGlnLeuArgMet	80
Dp	193	GAATCTATTACTTTGTGGACAGTTGGCTCCAAATTCATCAGCCACACTGAGAAATG	252
Oy	81	SerPheIleValPheSerThrArgIyIleThrIleuMetIysLeuThngIuaSPArgIu	100
Dp	253	TCTCTTATTTGTTTCTCCACCGAGGAAACAACCTTATGAAATCAGAGAAAGACAGAA	312
Oy	101	GlnIleArgGlnGlyLeuGluGlnLeuGlnIlyValLeuProGlyGlyAspThrTyrMet	120
Dp	313	CAAAATCGTCMAAGCCCTTAGAAGAACTCCGAAAGTTCGCCAGAGGGAGCACTTAATG	372
Oy	121	HisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArg	140
Dp	373	CATGAGAGATTTGAAAAGGCGCACTGACGAGATTTTATGAAAACAGACAGGGTAAAGG	432
Oy	141	ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPheTyr	160
Dp	433	ACAGCCAGCGTCATCATTTGCTTGAATGATGAGAACTCCATGAAGATCTTTTCTAT	492
Oy	161	SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal	180
Dp	493	TCAGAGGGAGGCTAATAGTCTCCAGATCTTGGATGCAATGTTTACTGTGGTGAGTG	552
Oy	181	IlyAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerIysAspHisValPhePro	200
Dp	553	AAAGATTTCAATAGACACAGCTGGCCCGGATTCGGGACAGTAAAGATCATGTGTTCCTC	612
Oy	201	ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuIlyIysSerCys	220
Dp	613	GTGATATCAGGCTTTCAAGCTCTGCAGAGCATCATCCACTCAATTTTGAAAGATCTCTGC	672
Oy	221	IleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGlySerPheGlnValVal	240
Dp	673	ATCGAAATTTTACACACTGAACCTCCACAAATGTGACAGGAGATCTATTCAAAGTGTCT	732
Oy	241	ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheIys	260
Dp	733	GTGAGAGGAAACGGCTTCCGACATGCCGCCCACTGAGACAGGCTCTTGCAGCTTCAAG	792
Oy	261	IleAsnAspSerValThrLeuAsnGluIysProPheSerValGluAspThrTyrLeuLeu	280
Dp	793	ATCAATATACCTCGGTCACTCATATGAGAGCCCTTTCTGTGGAAAGATATTATTACTG	852
Oy	281	CysProAlaProIleLeuIysGlyValAlaGlyMetIysAlaAlaLeuGlnValSerMetAsn	300
Dp	853	TGTCCACGGCTATCTTAAAGAAAGTTGACATGAAGAGTGCACTCCAGGTGACGATAC	912
Oy	301	AspGlyLeuSerPheIleSerSerSerValIleIleIleThrThrHisCysSerAspGly	320
Dp	913	GATGGCTCTCTTTTATCTCCAGTTGTGTCAATCATCACACACACACTGTTCTGAGGCT	972

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US-10-038-307-13
? Sequence 13, Application US/10038307
? Publication NO. US20030134786A1
? GENERAL INFORMATION:
? APPLICANT: James B. ROTTMAN
? APPLICANT: Theresa L. O'KEEFE
? APPLICANT: Engin OZKAYNAK
? APPLICANT: Judith J. HEALEY
? TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
? FILE REFERENCE: 7853-253-999
? CURRENT APPLICATION NUMBER: US/10/038.307
? CURRENT FILING DATE: 2002-06-28
? NUMBER OF SEQ ID NOS: 26
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 13
? LENGTH: 1650
? TYPE: DNA
? ORGANISM: Homo sapiens
US-10-038-307-13

```

**Alignment Scores:**

Pred. No.:	1,93e+204	Length:	1650
Score:	1650.00	Matches:	319
Percent Similarity:	99.38%	Conservative:	0
Best Local Similarity:	99.38%	Mismatches:	2
Query Match:	86.21%	Indels:	0
DB:	15	Gaps:	0

US-09-970-076-2 (1-368) X US-10-038-307-13 (1-1650)

QY	1	MetAlaThrAlaGlnArgArgAlaLeuGluGlyLeuGlyPheGlnIleProLeuSerLeuAlaThr	20
DB	1	ATGGCCACGGCGGAGGAGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTGGCCACT	60
QY	21	LeuValLeuIleCysAlaGlyGlnGlyGlyArgArgGluAspGlyGlyProAlaCysTyr	40
DB	61	CTGGTGTCTACTCGGCCCGGGGACAGGGGGAGCGACAGAGAGATGGGGGGTCCAGCTGTAC	120
QY	41	GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTPAsn	60
DB	121	GGGGATTGACCTGTACTTCTCAATTTGGACAATCGAGAAATGTGCTGCACACTGGAAAT	180
QY	61	GluIleTyrTyrPheValGlnGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet	80
DB	181	GAATCTATTACTTGTGTGAGACAGTTGGCTCCCAATTCATCAGCCCACTTGAATG	240
QY	81	SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu	100
DB	241	TCTTTATTGTGTTTCCACCCGAGGACCAACTTAAAGAACTGACAGAGACAGAGAA	300
QY	101	GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrMet	120
DB	301	CAATCCGTCMAAGCCCTTGAAGAACTCCAGAAAGTTCTCCAGAGAGAGACACTTAATG	360
QY	121	HisGluGlyPheGluArgLysSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArg	140
DB	361	CAATGAGATTGAAAGGGCCAGTACGACAGATTATTATGAAACAGACMAAGGTTACAG	420
QY	141	ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPheTyr	160
DB	421	ACAGCCAGCTCATCTTGTCTTGTGACTGAGAGAACTCCATGAAAGATCTCTTTTCTAT	480
QY	161	SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal	180
DB	481	TCAGAGAGGGAGGCTAAATAGTCTCGAAGTCTTGGTGAATTTGTTACTGTGTGGTGTG	540
QY	181	LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro	200
DB	541	AAAGATTTCATATAGACACAGCTGGCCCGGATTTGGCGACATGAAAGATCATGTCTTCCC	600
QY	201	ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys	220
DB	601	GTAATGACCGGCTTTCAGGCTCTGCAAGGCAATCATCACTCAATTTTGAAGAAATCTCTGC	660

```

QY 221 IleguileleuAlaGluProSerThrIleCyAlaGlyGlySerPheGlnVal 240
DB 661 ATCGAAATTTCTTGACGCTGACACCATCCACCATATGTGGAGAGTCAATTTAAAGTTGTC 720
QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCySerPheLys 260
DB 721 GTGAGAGGAAACGGCTTCGACATGCCGCAACGTGACAGGGTCTCTGACAGCTTCAAG 780
QY 261 IleAsnAspSerValThrLeuAsnGlyLysProPheSerValGlnAspThrTyrlleuLeu 280
DB 781 ATCAATGACTCGGTGACACTCAATGAGAACCCCTTTCTGTGAAGATTAATTTACTG 840
QY 281 CysProAlaProIleLeuLysGlyValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
DB 841 TGTCCAGCGCTTATCTTAAGAAGTGGCATGAAGGTCAGCTCAGGTCAGCATGAAC 900
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCySerAspGly 320
DB 901 GATGGCCTCTCTTTATCTCCAGTTCTGTGCATCATCACACACACACTGTTCTCCCAA 960
QY 321 Ser 321
DB 961 TCT 963

RESULT 11
; Sequence 15, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: James B. ROTTMAN
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1650
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-15

Alignment Scores:
Pred. No.: 1,936-204 Length: 1650
Score: 1650.00 Matches: 319
Percent Similarity: 99.38% Conservative: 0
Best Local Similarity: 99.38% Mismatches: 2
Query Match: 86.21% Indels: 0
DB: 15 Gaps: 0

US-09-970-076-2 (1-366) x US-10-038-307-15 (1-1650)
QY 1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnThrLeuSerLeuAlaThr 20
DB 1 ATGGCCAGCGCGGAGCGGAGAGCCCTCGGCATCGGCTTCAGTGCCTCTCTTTGGCCACT 60
QY 21 LeuValIleuIleCyArgAlaGlyGlnGlyArgArgGluAspGlyGlyProAlaCySerTy 40
DB 61 CTGGGCTCTATCTGCGCGGCAAGGGGACGACGAGGAGAAAGGGGGTCTCAAGCTGCTAC 120
QY 41 GlyGlyPheAspLeuTyrlleuLeuAspLysSerGlySerValLeuHisIleThrAsn 60
DB 121 GCGGGAATTTGACCTGTACTTTCATTTTGGACAAATCAGAAAGTGTCTGACACACAGTGAAT 180
QY 61 GluIleTyrlleuPheValGluGlnLeuAlaHisIlyPheIleSerProGlnLeuArgMet 80
DB 181 GAAATCTATTACTTTGTGGAAACAGTTGGCTCAAAATTCATCAGCCCAAGTTGAGAAATG 240
QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGlnAspArgGlu 100

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DB 241 TCTTTATTTGTTTCTCCACCGAGAACCACTTAATGAACCTACAGAGACAGAGA 300
QY 101 GlnIleArgGlnGlyLeuGlnGlyLeuGlnLysValIleuProGlyValAspThrTyrlleu 120
DB 301 CAATCCCTTCAGAGGCTTGAAGAACTCCAGAAAGTTCTCCAGAGGAGAACCTTAACATG 360
QY 121 HisGluGlyPheGluArgAlaSerGlyGlnIleTyrlleuArgLysAsnArgGlnIlyTyrlleu 140
DB 361 CATGAAGATTTGAAGAGCCAGTGAAGATTTATTTGAAGAACAGACAGAGGTACAG 420
QY 141 ThrAlaSerValIleIleAlaLeuThrAspGlyGlyLeuHisGluAspLeuPhePheTyrlleu 160
DB 421 ACAGCCACGTCATATGCTTTGATGATGAGAACTCCATGAAGATCTCTTTTCTAT 480
QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrlleuValGlyVal 180
DB 481 TCAGAGAGGAGGCTTAATAGGCTTCGAGATCTTGTCAAATTTACTGTGTGTGTG 540
QY 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
DB 541 AAAGATTCATAGAGACACAGCTGACCGGAGTGGCAAGAGTAAAGATCATGTGTTCC 600
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220
DB 601 GTGAATGACGGCTTCAAGGCTCTGCAAGCATCATCCACTCAATTTTGAAGAGTCTGTC 660
QY 221 IleguileleuAlaGluProSerThrIleCyAlaGlyGlySerPheGlnVal 240
DB 661 ATCGAAATTTCTTGACGCTGACACCATCCACCATATGTGGAGAGTCAATTTAAAGTTGTC 720
QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCySerPheLys 260
DB 721 GTGAGAGGAAACGGCTTCGACATGCCGCAACGTGACAGGGTCTCTGACGCTTCAAG 780
QY 261 IleAsnAspSerValThrLeuAsnGlyLysProPheSerValGlnAspThrTyrlleuLeu 280
DB 781 ATCAATGACTCGGTGACACTCAATGAAGACCCCTTTCTGTGAGAGATTAATTTACTG 840
QY 281 CysProAlaProIleLeuLysGlyValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
DB 841 TGTCCAGCGCTTATCTTAAGAAGTGGCATGAAGTGCATCCAGGTCAGCATGAAC 900
QY 301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCySerAspGly 320
DB 901 GATGGCCTCTCTTTATCTCCAGTTCTGTGCATCATCACACACACACTGTTCTCCCAA 960
QY 321 Ser 321
DB 961 TCT 963

RESULT 12
; Sequence 13, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1650
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-13

Alignment Scores:

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Db 541 AAGATTTCATAGACACAGCTGCCCGATTCGGCAGTAGAATCATGTGTTCCC 600  
Qy 201 ValaenapglPheglAlaleuInglYlelleHeserIleleuYalysSerCys 220  
Db 601 GTGAATGACGGCTTTCAGGCTTCGAGGACATCATCTCAATTTTGAAGAAGTCTGC 660  
Qy 221 IleguileleuAlaAlaGluProSerThrIleCySaAlaGlyGluSerPheglInVal 240  
Db 661 ATCGAATTTCTAGACAGCTGAACCATTCACATATGTGCGAGAGATCATTTCAAGTTGTC 720  
Qy 241 ValaArgGlyAenGlyPheArgHleAlaArgAenValaAspArgValleuCySerPheIys 260  
Db 721 GTGAGAGGAAACGGCTTCGACATGCTCCGCAACGTGACAGGCTCTTCGACGTTCAAG 780  
Qy 261 IleAenApsSerValThreleuAenGlyuysPhePheSerValGluAspThrTyreleu 280  
Db 781 ATCAATGACTCGGTCACTCAATGAGAACGCTTTTGTGGAAGATCTATTATTACG 840  
Qy 281 CysProAlaProIleleuYalGlyuAlaGlyuAlaAlaGluInValSerMetAen 300  
Db 841 TGTCCAGCCCTATCTTAATAAGATGGCATGAAGCTGCACTCAGTCCAGTCAAGTCAAC 900  
Qy 301 AspglyleuSerPheIleSerSerSerValIlelleThrThrThiCySerAspGly 320  
Db 901 GATGACCTCTCTTTATCTCCAGTTCGTGTCATCATCACACACACTGTTCTCCAA 960  
Qy 321 Ser 321  
Db 961 TCT 963  
RESULT 14  
US-10-038-307-23  
; Sequence 23, Application US/10038307  
; Publication No. US20030134786A1  
; GENERAL INFORMATION:  
; APPLICANT: James B. ROTTMAN  
; APPLICANT: Theresa L. O'KEEFE  
; APPLICANT: Engin OZKAYNAK  
; APPLICANT: Judith J. HEALEY  
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
; FILE REFERENCE: 7853-253-999  
; CURRENT APPLICATION NUMBER: US/10/038,307  
; CURRENT FILING DATE: 2002-06-28  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 1056  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-038-307-23  
Alignment Scores:  
Pred. No.: 1.23e-204 Length: 1056  
Score: 1649.00 Matches: 318  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 86.15% Indels: 0  
DB: 15 Gaps: 0  
US-09-970-076-2 (1-368) x US-10-038-307-23 (1-1056)  
Qy 1 MetAlaThrAlaGluArgAlaAlaGluGlyIleGlyPheGlnTrpLeuSerIleuAlaThr 20  
Db 13 ATGGCCACCGCGCGAGCGGAGACCCCTCGGCATCGGCTTCACATGCTCTCTTGGCCACT 72  
Qy 21 LeuValleuIleCyAlaGlyInglYalArgArgGluAenGlyGlyProAlaCysTyx 40  
Db 73 CTGGGCTCATCTGGCCCGGCAAGGGGAGACGAGGAGAGAGGGGCTCAACCTGCTAC 132  
Qy 41 GlyGlyPheAspLeuTyPheIleleuAenGlySerGlySerValleuHisIstrpAen 60  
Db 133 GGGCGATTTCAGCTGATCTTTTGAACAAATCAGAAAGTGTGTGACCACTGGAAAT 192

Qy 61 GluIleTyTyPheValGluGluInleuAlaHisIysPheIleSerProGluInleuArgMet 80  
Db 193 GAATCTATTACTTGTGGAAACAGTGTGGCTCAAAATTCATCAGCCCAAGTTGGAATG 252  
Qy 81 SerPheIleValPheSerThrArgGlyThrThreleuMetIysleuThrGluAspArgGlu 100  
Db 253 TCTTTATTGTTTCTTCCACCCGAGAAACAACCTTAAAGAACTGACAGAAACAGAGAA 312  
Qy 101 GlnIleArgGlnGlyleuGluInleuGlnIysValleuProGlyGlyAspThrTyMet 120  
Db 313 CAATCCCTCAAGGCTTGAAGAACTCCAGAAAGTTCTGCGAGGAGAGACCTTACATG 372  
Qy 121 HisGluGlyPheGluArgAlaSerGluGlnIleTyTyGlyuAspArgGlnGlyTyArg 140  
Db 373 CATGAAGATTTGAAGAGCCGATGACGANTTTATTTGAAAACAGCAAGAGATACAGG 432  
Qy 141 ThrAlaSerValIlelleAlaIleuThrAspGlyGluIleuHisGluAspLeuPhePheTy 160  
Db 433 ACAGCCAGCTCATCATGCTTTGACTGATGAGAACTCCATGAAGATCTCTTTTCTAT 492  
Qy 161 SerGluArgGluAlaAspArgSerArgAspLeuGlyAlaIleValTyCyAlaGlyVal 180  
Db 493 TCAGAGAGGAGGCTTAATAGCTTCGAGATCTTGTCAAATTTTACTGTGTGTGTG 552  
Qy 181 LysAspPheAenGluThrGluInleuAlaArgIleAlaAspSerLysAspHisValPhePro 200  
Db 553 AAGATTTCATAGACACACAGCTGCCCGGATGTGGGACAGTAAGATCATGTGTTCCC 612  
Qy 201 ValaenapglYpheglAlaleuInglYlelleHeserIleleuYalysSerCys 220  
Db 613 GTGAATGACGGCTTTCAGGCTTCGCAAGCATCATCCACTCAATTTTGAAGAAGTCTGC 672  
Qy 221 IleguileleuAlaAlaGluProSerThrIleCySaAlaGlyGluSerPheglInVal 240  
Db 673 ATCGAATTTCTAGACAGCTGAACCATCCACATATGTGAGAGAGATCTCAATTCAGTTC 732  
Qy 241 ValaArgGlyAenGlyPheArgHleAlaArgAenValaAspArgValleuCySerPheIys 260  
Db 733 GTGAGAGAAACGGCTTCGACATGCCGCAACGTGACAGGCTCTTCGACGTTCAAG 792  
Qy 261 IleAenApsSerValThreleuAenGlyuysPhePheSerValGluAspThrTyreleu 280  
Db 793 ATCAATGACTCGGTCACTCAATGAGAAAGCTTTTGTGGAAGATCATATTATTACG 852  
Qy 281 CysProAlaProIleleuYalGlyuAlaGlyuAlaAlaGluInValSerMetAen 300  
Db 853 TGTCCAGCGCTTATCTTAATAAGATGGCATGAAGCTGCACTCAGGTCCAGTCAAGTCAAC 912  
Qy 301 AspglyleuSerPheIleSerSerSerValIlelleThrThrThiCySer 318  
Db 913 GATGACCTCTCTTTATCTCCAGTTCGTGTCATCATCACACCACTGTAAGC 966  
RESULT 15  
US-10-201-292-23  
; Sequence 23, Application US/10201292  
; Publication No. US20030144193A1  
; GENERAL INFORMATION:  
; APPLICANT: James B. ROTTMAN  
; APPLICANT: Theresa L. O'KEEFE  
; APPLICANT: Engin OZKAYNAK  
; APPLICANT: Judith J. HEALEY  
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
; FILE REFERENCE: 7853-253-999  
; CURRENT APPLICATION NUMBER: US/10/201,292  
; CURRENT FILING DATE: 2003-02-14  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 1056  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-201-292-23

## Alignment Scores:

Pred. No.:	1,236-204	Length:	1056
Score:	1649.00	Matches:	318
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	86.15%	Indels:	0
DB:	15	Gaps:	0

US-09-970-076-2 (1-366) x US-10-201-292-23 (1-1056)

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QY      1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnITrPheSerLeuAlaThr 20
      13 ATGGCCAGCGGAGGAGGAGACCTCGGCATCGGCTTCAGTGGCTCTTTGGCCACT 72
QY      21 LeuValLeuIleCyAlaGlyGlnGlyIleValArgGluAspGlyGlyProAlaCysTrp 40
      73 CTGGTGCCTCATCTGGCGCGGGAAGGGAGCGCAGAGAGATGGGGGTCCAGCCTGTAC 132
QY      41 GlyGlyPheAspLeuTrpPheIleLeuAspLysSerGlySerValLeuHisITrPasn 60
      133 GCGGATTTGACCTGTACTTCATTTTGACAATCAGAGAGTGTCTGCACCACTGAAAT 192
QY      61 GluIleTrpTrpPheValGluGlnLeuAlaHisLysPheIleSerProGlnLeuArgMet 80
      193 GAAATCTATTACTTTGTGAAACAGTTGGCTCAAAATTCATCAGCCACAGTTGAAGATG 252
QY      81 SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
      253 TCCTTATTTGTTTTCCTCCAGCGAGAACCTTATGAACTGACAGAAAGACAGAA 312
QY      101 GlnIleArgGlnGlyLeuGlnGlnLeuGlnLysValLeuProGlyGlyAspThrTrpMet 120
      313 CAAATCCGTCAGAGCCCTAGAGAACTCCAGAAAGTTCTGCAGAGAGACACTTACATG 372
QY      121 HisGluGlyPheGluArgAlaSerGlnGlnIleTrpTrpGluAsnArgGlnGlyTrpArg 140
      373 CATGAAGGATTTGAAAGGGCCAGTGAAGCATTTATGAAACAGCAAGGGTACAGG 432
QY      141 ThrAlaSerValIleIleAlaLeuThrAspGlyGlnLeuHisGluAspLeuPhePheTrp 160
      433 ACAGCCAGCGTCATCATTTGCTTTGACTGATGAGAACTCCATGAAGATCTCTTTTCAT 492
QY      161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTrpCysValGlyVal 180
      493 TCAGAGAGGAGGCTTAATAGCTCGAGATCTTGGTCATTTACTGATGTGTGTG 552
QY      181 LysAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
      553 AAAGATTTCAATGAACACAGCTGGCCCGGATTCGGACAGTAAAGATCATGTGTTCC 612
QY      201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSerCys 220
      613 GTGAATGACGGCTTTCAGGCTCTGCAGGCAATCCACTCAATTTTGAAGAGTCCCTGC 672
QY      221 IleGlnIleLeuAlaIleGluProSerThrIleCysAlaGlyLysSerPheGlnValVal 240
      673 ATCGAAATTTAGCAGCTGAACCATCCACATATGTGCAGAGAGTCAATTCAGTGTGC 732
QY      241 ValArgGlyAsnGlyPheArgHisAlaIleArgAsnValAspArgValLeuCysSerPheLys 260
      733 GTGAGAGGAAACGGCTTCGACATGCCGCAACGTGACAGGGTCTCTGCAGCTTCAAG 792
QY      261 IleAsnAspSerValThrLeuAsnGlnLysProPheSerValGluAspThrTrpLeuLeu 280
      793 ATCAATGACTCGGTACACTCATAGAGAGCCCTTTCTGTGAGAGATCACTTATTACTCG 852
QY      281 CysProAlaProIleLeuLysGlnValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
      853 TGTCCAGGCGCCATCTTAAAGAACTTGGCATGAAGCTGCACCTCAGGTCAAGCATGAAC 912
QY      301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSer 318
      913 GATGGCCTCTCTTTATCTCCAGTTCTGTGCATCATCACCAACACACTGTAGC 966
DB
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Search completed: June 22, 2004, 08:10:30  
Job time : 571.154 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: June 21, 2004, 13:39:51 ; Search time 13.8962 Seconds

(without alignments)  
1367.166 Million cell updates/sec

Title: US-09-970-076-2

Perfect score: 1914  
Sequence: 1 MATBRRLAGTGFQWLSLAT.....VIKEVPPPAESENKIK 368

## Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Database :

Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/1aa/PCUTS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	166	8.7	1155	1 US-08-286-889-46	Sequence 46, Appl
2	166	8.7	1155	1 US-08-485-618-46	Sequence 46, Appl
3	166	8.7	1155	1 US-08-362-652-46	Sequence 46, Appl
4	166	8.7	1155	2 US-08-605-672-46	Sequence 46, Appl
5	166	8.7	1155	2 US-08-482-293A-46	Sequence 46, Appl
6	166	8.7	1155	2 US-08-943-363-46	Sequence 46, Appl
7	166	8.7	1155	3 US-09-193-043-46	Sequence 46, Appl
8	166	8.7	1155	4 US-09-688-307A-46	Sequence 46, Appl
9	166	8.7	1155	4 US-09-350-259-46	Sequence 46, Appl
10	166	8.7	1161	1 US-08-485-618-53	Sequence 53, Appl
11	166	8.7	1161	1 US-08-362-652-53	Sequence 53, Appl
12	166	8.7	1161	2 US-08-605-672-53	Sequence 53, Appl
13	166	8.7	1161	2 US-08-482-293A-53	Sequence 53, Appl
14	166	8.7	1161	3 US-08-943-363-53	Sequence 53, Appl
15	166	8.7	1161	3 US-09-193-043-53	Sequence 53, Appl
16	166	8.7	1161	4 US-09-688-307A-53	Sequence 53, Appl
17	166	8.7	1161	4 US-09-350-259-53	Sequence 53, Appl
18	159.5	8.3	1151	1 US-08-286-889-37	Sequence 37, Appl
19	159.5	8.3	1151	1 US-08-485-618-37	Sequence 37, Appl
20	159.5	8.3	1151	1 US-08-362-652-37	Sequence 37, Appl
21	159.5	8.3	1151	2 US-08-605-672-37	Sequence 37, Appl
22	159.5	8.3	1151	2 US-08-482-293A-37	Sequence 37, Appl
23	159.5	8.3	1151	2 US-08-943-363-37	Sequence 37, Appl
24	159.5	8.3	1151	3 US-09-193-043-37	Sequence 37, Appl
25	159.5	8.3	1151	4 US-09-688-307A-37	Sequence 37, Appl
26	159.5	8.3	1151	4 US-09-350-259-37	Sequence 37, Appl
27	159.5	8.3	1161	1 US-08-173-497-2	Sequence 2, Appl

28	159.5	8.3	1161	1 US-08-286-889-2	Sequence 2, Appl
29	159.5	8.3	1161	1 US-08-485-618-2	Sequence 2, Appl
30	159.5	8.3	1161	1 US-08-362-652-2	Sequence 2, Appl
31	159.5	8.3	1161	1 US-08-605-672-2	Sequence 2, Appl
32	159.5	8.3	1161	1 US-08-482-293A-2	Sequence 2, Appl
33	159.5	8.3	1161	1 US-08-943-363-2	Sequence 2, Appl
34	159.5	8.3	1161	2 US-08-605-672-2	Sequence 2, Appl
35	159.5	8.3	1161	2 US-08-482-293A-2	Sequence 2, Appl
36	159.5	8.3	1161	2 US-08-943-363-2	Sequence 2, Appl
37	159.5	8.3	1161	2 US-08-605-672-2	Sequence 2, Appl
38	159.5	8.3	1161	2 US-08-482-293A-2	Sequence 2, Appl
39	159.5	8.3	1161	2 US-08-943-363-2	Sequence 2, Appl
40	159.5	8.3	1161	2 US-08-605-672-2	Sequence 2, Appl
41	159.5	8.3	1161	2 US-08-482-293A-2	Sequence 2, Appl
42	159.5	8.3	1161	2 US-08-943-363-2	Sequence 2, Appl
43	159.5	8.3	1161	3 US-09-193-043-2	Sequence 2, Appl
44	159.5	8.3	1161	3 US-09-688-307A-2	Sequence 2, Appl
45	159.5	8.3	1161	3 US-09-350-259-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-08-286-889-46  
Sequence 46, Application US/08286889  
Patent No. 5470953  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Mich  
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Seair Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/286, 889  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: P38,659  
REFERENCE/DOCKET NUMBER: 27866/32168  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1155 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-286-889-46

Query Match 8.7% Score 166; DB 1; Length 1155;  
Best Local Similarity 28.2%; Pred. No. 7.6e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;  
37 PACYV-GPDLYFLDKSGSV-LHHNNEIYVVEQLAHKFIISPOLRMSFVISTRTITMK 94

Db 144 PEGCGEMDIAFLIDSGSIDQSDFTQKDFVAKLMQLASTSTSFSLMOYSNLIKTHFT 203  
Qy 95 LTEDR-----EQIROGLEELQKVLPGGDTYMHGFERASBOIYYENRGYRTA-SVIAL 148  
Db 204 PTEFKSSLSPOSIVDAIVQLO-----GLTYTASGIQKVVELFHSKNGARKSACKILIVI 258  
Qy 149 TDGEIHEDLFFYSE--REANRSRDLGAIYVCVKD-FNE-TOLARI-----ADSKDHVF 199  
Db 259 TDGQKFRDPLEYHRHVIPEAKA---GIIRYAIQGDVAFREPTALQELNLTGSAFSQDHVF 315  
Qy 200 PVNDGFALOGIHSILKSCIEILAAPSTICAGESFQVVRNGNFRHARNVD 253  
Db 316 KVGN-FVALRSIQROIQER---IFALRGTESSSSSFQHEMSQEGESSALSMD 364

## RESULT 2

US-08-485-618-46  
; Sequence 46, Application US/08485618  
; Patent No. 5728533  
; GENERAL INFORMATION:  
; APPLICANT: Gallatin, W. Michael  
; APPLICANT: Van der Vlieten, Monica  
; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 South Wacker Drive, 6300 Seear Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485, 618  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/173,497  
; FILING DATE: 23-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/286,889  
; FILING DATE: 5-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/362,652  
; FILING DATE: 21-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams Jr., Joseph A.  
; REGISTRATION NUMBER: 38,659  
; REFERENCE/DOCKET NUMBER: 27866/32797  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; TELEFAX: 312-474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 46:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1155 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-485-618-46

Query Match 8.7%; Score 166; DB 1; Length 1155;

Best Local Similarity 28.2%; Pred. No. 7.6e-09;

Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

Qy 37 PACYG-GFDLYFIIDKSGSV-LHMHNEIYFVEQLAHFISPOLRMSFIVSTGTLMK 94  
Db 144 PEGCGEMDIAFLIDSGSIDQSDFTQKDFVAKLMQLASTSTSFSLMOYSNLIKTHFT 203

Qy 95 LTEDR-----EQIROGLEELQKVLPGGDTYMHGFERASBOIYYENRGYRTA-SVIAL 148  
Db 204 PTEFKSSLSPOSIVDAIVQLO-----GLTYTASGIQKVVELFHSKNGARKSACKILIVI 258  
Qy 149 TDGEIHEDLFFYSE--REANRSRDLGAIYVCVKD-FNE-TOLARI-----ADSKDHVF 199  
Db 259 TDGQKFRDPLEYHRHVIPEAKA---GIIRYAIQGDVAFREPTALQELNLTGSAFSQDHVF 315  
Qy 200 PVNDGFALOGIHSILKSCIEILAAPSTICAGESFQVVRNGNFRHARNVD 253  
Db 316 KVGN-FVALRSIQROIQER---IFALRGTESSSSSFQHEMSQEGESSALSMD 364

## RESULT 3

US-08-362-652-46  
; Sequence 46, Application US/08362652  
; Patent No. 5766850  
; GENERAL INFORMATION:  
; APPLICANT: Gallatin, W. Michael  
; APPLICANT: Van der Vlieten, Monica  
; TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit  
; NUMBER OF SEQUENCES: 93  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 South Wacker Drive, 6300 Seear Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/362,652  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/173,497  
; FILING DATE: 23-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/286,889  
; FILING DATE: 5-AUG-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams Jr., Joseph A.  
; REGISTRATION NUMBER: 38,659  
; REFERENCE/DOCKET NUMBER: 27866/32391  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; TELEFAX: 312-474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 46:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1155 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-362-652-46

Query Match 8.7%; Score 166; DB 1; Length 1155;

Best Local Similarity 28.2%; Pred. No. 7.6e-09;

Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

Qy 37 PACYG-GFDLYFIIDKSGSV-LHMHNEIYFVEQLAHFISPOLRMSFIVSTGTLMK 94  
Db 144 PEGCGEMDIAFLIDSGSIDQSDFTQKDFVAKLMQLASTSTSFSLMOYSNLIKTHFT 203  
Qy 95 LTEDR-----EQIROGLEELQKVLPGGDTYMHGFERASBOIYYENRGYRTA-SVIAL 148  
Db 204 PTEFKSSLSPOSIVDAIVQLO-----GLTYTASGIQKVVELFHSKNGARKSACKILIVI 258  
Qy 149 TDGEIHEDLFFYSE--REANRSRDLGAIYVCVKD-FNE-TOLARI-----ADSKDHVF 199

Db 259 TDGQFRDPLEYRHYIPEAEKA---GIRYALGVDAFAPEPALQELMTIGSAPQDHVF 315  
QY 200 PVDGFOALQGIHSHILKKSCEIILAEPTICAGESFOVVVNGGFRHARVD 253  
Db 316 KVGK-FVALRSTIQIOEK-----IFALGCTESSRSSSFQHEMSQGFSSALSM 364

## RESULT 4

US-08-605-672-46  
Sequence 46, Application US/08605672  
Patent No. 5817515  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum  
STREET: 233 South Wacker Drive, 6300 Seer Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/605,672  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1155 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-605-672-46

Query Match 8.7%; Score 166; DB 2; Length 1155;  
Best Local Similarity 28.2%; Pred. No. 7.6e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;  
QY 37 PACYV-GPDLYFILDKSGSV-LHNNELIYFVEQLAHKFIISPOLMSFVSTRTGTTLMK 94  
Db 144 PECPOEMDIAPLIDGSSIDSDPTOMKDFKALMGQLASTSTSFSLMOYSNLIKTHFT 203  
QY 95 LTEDR-----EQRGLLELQKVLPGCDTYMHEGFERASEQIYYENRGYRTA-SVIAL 148  
Db 204 FTEFKSSLSPOSLVDALVOLQ-----GLTYASGIQVKVKEIPHSKNGARKSAKKILIVI 258  
QY 149 TDGELHELDLFYSE--REANRSRDLGAIYVCVYKD-FNE-TOLARI-----ADSKDHVF 199  
Db 259 TDGQFRDPLEYRHYIPEAEKA---GIRYALGVDAFAPEPALQELMTIGSAPQDHVF 315

QY 200 PVDGFOALQGIHSHILKKSCEIILAEPTICAGESFOVVVNGGFRHARVD 253  
Db 316 KVGK-FVALRSTIQIOEK-----IFALGCTESSRSSSFQHEMSQGFSSALSM 364

## RESULT 5

US-08-482-293A-46  
Sequence 46, Application US/08482293A  
Patent No. 5831029  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum  
STREET: 233 South Wacker Drive, 6300 Seer Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,293A  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1155 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-482-293A-46

Query Match 8.7%; Score 166; DB 2; Length 1155;  
Best Local Similarity 28.2%; Pred. No. 7.6e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;  
QY 37 PACYV-GPDLYFILDKSGSV-LHNNELIYFVEQLAHKFIISPOLMSFVSTRTGTTLMK 94  
Db 144 PECPOEMDIAPLIDGSSIDSDPTOMKDFKALMGQLASTSTSFSLMOYSNLIKTHFT 203  
QY 95 LTEDR-----EQRGLLELQKVLPGCDTYMHEGFERASEQIYYENRGYRTA-SVIAL 148  
Db 204 FTEFKSSLSPOSLVDALVOLQ-----GLTYASGIQVKVKEIPHSKNGARKSAKKILIVI 258  
QY 149 TDGELHELDLFYSE--REANRSRDLGAIYVCVYKD-FNE-TOLARI-----ADSKDHVF 199  
Db 259 TDGQFRDPLEYRHYIPEAEKA---GIRYALGVDAFAPEPALQELMTIGSAPQDHVF 315  
QY 200 PVDGFOALQGIHSHILKKSCEIILAEPTICAGESFOVVVNGGFRHARVD 253

Db 316 KVGK-FVALRSIQIOEK-----IPALGTESSSSSFQHEMSQGFSSALSMD 364

RESULT 6  
US-08-943-363-46  
Sequence 46, Application US/08943363  
Patent No. 5837478  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
TITLE OF INVENTION: No. 5837478 Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Sear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,363  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1155 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-943-363-46

Query Match 8.7%; Score 166; DB 2; Length 1155;  
Best Local Similarity 28.2%; Pred. No. 7.6e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

Qy 37 PACYG-GFDLYFLIDKSGSV-LHHMNEIYFVEQLAHKFIISPOLMSFIVSTGTTLMK 94  
Db 144 PECQGMEDIAFLIDSGSIDQSDPTQKDFVKALMGQLASTSTSFSLMOTSNILKTHFT 203  
Qy 95 LTEDR-----EQLRGLEELQKVLPGDPTVMHEGFERASEQIYYENRGYRTA-SVIAL 148  
Db 204 FTEFKSSLSPOSLVDALVQLQ-----GLTYTASGIQKVVKELFHSKNGARSAKKILIVI 258  
Qy 149 TDGELHEDLFPYSE--REANRSRDGAIVYCVGYKD-FNE-TOLARI-----ADSKDHVF 199  
Db 259 TDGQKFRDPLEYRHYVPEAEKA---GIIRYALGVGDAPREPTALQELNTIGSAPSQDHVF 315  
Qy 200 PVNDGFQALOGIHSILKSCIEIILAEPTICAGSFQVYVVRNGGFRHARNVD 253  
Db 316 KVGK-FVALRSIQIOEK-----IPALGTESSSSSFQHEMSQGFSSALSMD 364

Db 316 KVGK-FVALRSIQIOEK-----IPALGTESSSSSFQHEMSQGFSSALSMD 364

RESULT 7  
US-09-193-043-46  
Sequence 46, Application US/09193043  
Patent No. 6251395  
GENERAL INFORMATION:  
APPLICANT: Gallatin, Michael W.  
TITLE OF INVENTION: No. 6251395 Human 2  
FILE REFERENCE: 27866/35004  
CURRENT APPLICATION NUMBER: US/09/193,043  
PRIOR FILING DATE: 1998-11-16  
EARLIER APPLICATION NUMBER: 08/173,497  
EARLIER FILING DATE: 1993-12-23  
EARLIER APPLICATION NUMBER: 08/286,889  
EARLIER FILING DATE: 1994-08-05  
EARLIER APPLICATION NUMBER: 08/362,652  
EARLIER FILING DATE: 1994-12-21  
EARLIER APPLICATION NUMBER: 08/943,363  
EARLIER FILING DATE: 1997-10-03  
NUMBER OF SEQ ID NOS: 114  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO: 46  
LENGTH: 1155  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-193-043-46

Query Match 8.7%; Score 166; DB 3; Length 1155;  
Best Local Similarity 28.2%; Pred. No. 7.6e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

Qy 37 PACYG-GFDLYFLIDKSGSV-LHHMNEIYFVEQLAHKFIISPOLMSFIVSTGTTLMK 94  
Db 144 PECQGMEDIAFLIDSGSIDQSDPTQKDFVKALMGQLASTSTSFSLMOTSNILKTHFT 203  
Qy 95 LTEDR-----EQLRGLEELQKVLPGDPTVMHEGFERASEQIYYENRGYRTA-SVIAL 148  
Db 204 FTEFKSSLSPOSLVDALVQLQ-----GLTYTASGIQKVVKELFHSKNGARSAKKILIVI 258  
Qy 149 TDGELHEDLFPYSE--REANRSRDGAIVYCVGYKD-FNE-TOLARI-----ADSKDHVF 199  
Db 259 TDGQKFRDPLEYRHYVPEAEKA---GIIRYALGVGDAPREPTALQELNTIGSAPSQDHVF 315  
Qy 200 PVNDGFQALOGIHSILKSCIEIILAEPTICAGSFQVYVVRNGGFRHARNVD 253  
Db 316 KVGK-FVALRSIQIOEK-----IPALGTESSSSSFQHEMSQGFSSALSMD 364

RESULT 8  
US-09-688-307A-46  
Sequence 46, Application US/09688307A  
Patent No. 6432404  
GENERAL INFORMATION:  
APPLICANT: Gallatin, Michael W.  
TITLE OF INVENTION: No. 6432404 Human Beta-2  
FILE REFERENCE: 27866/36646  
CURRENT APPLICATION NUMBER: US/09/688,307A  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: 09/193,043  
PRIOR FILING DATE: 1998-11-16  
PRIOR APPLICATION NUMBER: 08/605,672  
PRIOR FILING DATE: 1996-02-22  
PRIOR APPLICATION NUMBER: 08/173,497  
PRIOR FILING DATE: 1993-12-23  
PRIOR APPLICATION NUMBER: 08/286,889  
PRIOR FILING DATE: 1994-08-05  
PRIOR APPLICATION NUMBER: 08/362,652  
PRIOR FILING DATE: 1994-12-21  
PRIOR APPLICATION NUMBER: 08/943,363  
PRIOR FILING DATE: 1997-10-03

NUMBER OF SEQ ID NOS: 114  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 46  
LENGTH: 1155  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-688-307A-46

Query Match 8.7%; Score 166; DB 4; Length 1155;  
Best Local Similarity 28.2%; Pred. No. 7.6e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYG-GRDLYFLIDKSGSV-LHMHNEIYFVEQALAHKFIISPOLMSEFIVSTRTGTTLMK 94  
DB 144 PECQEQENDIAFLIDGSSSIDQSDPTQMKDFVKALMGQLASTSTSFSLMOYSNLIKTHFT 203  
QY 95 LTEDR-----EQIRQGLEELQKVLPGSDTYMHGFERASEQIYYENRGYRTA-SVIAL 148  
DB 204 FTEFKSSLSPOSLVDALVQLQ-----GLTYASGIQKVKELFHSKNGARKSAAKILIVI 258  
QY 149 TDGELHEDLFFYSE--REANRSRDGAIVYCVGVND-FNE-TOLARI-----ADSKDHVF 199  
DB 259 TDGQKFRPDLRYRHYIPEAEKA---GIRYALGVGDAREPFTALQELMTTISAPSQDHVF 315  
QY 200 PVNDGFOALOGIHSILKSCIEILAEPTICAGESFOVVVNGGFRHARVD 253  
DB 316 KVGK-FVALRSTQRIQEK-----IFALIGTSRSSSSSFQHEMSQEGFSSALSM 364

## RESULT 9

US-09-350-259-46  
Sequence 46, Application US/09350259  
Patent No. 6620915  
GENERAL INFORMATION:  
APPLICANT: Gallatin, Michael W.  
APPLICANT: Van der Vieren, Monica  
TITLE OF INVENTION: No. 6620915e1 Human 2  
FILE REFERENCE: 27866/35004  
CURRENT APPLICATION NUMBER: US/09/350,259  
FILING DATE: 1999-07-08  
EARLIER APPLICATION NUMBER: 09/193,043  
EARLIER FILING DATE: 1998-11-16  
EARLIER APPLICATION NUMBER: 08/173,497  
EARLIER FILING DATE: 1993-12-23  
EARLIER APPLICATION NUMBER: 08/286,889  
EARLIER FILING DATE: 1994-08-05  
EARLIER APPLICATION NUMBER: 08/362,652  
EARLIER FILING DATE: 1994-12-21  
EARLIER APPLICATION NUMBER: 08/943,363  
EARLIER FILING DATE: 1997-10-03  
NUMBER OF SEQ ID NOS: 114  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 46  
LENGTH: 1155  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-350-259-46

Query Match 8.7%; Score 166; DB 4; Length 1155;  
Best Local Similarity 28.2%; Pred. No. 7.6e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYG-GRDLYFLIDKSGSV-LHMHNEIYFVEQALAHKFIISPOLMSEFIVSTRTGTTLMK 94  
DB 144 PECQEQENDIAFLIDGSSSIDQSDPTQMKDFVKALMGQLASTSTSFSLMOYSNLIKTHFT 203  
QY 95 LTEDR-----EQIRQGLEELQKVLPGSDTYMHGFERASEQIYYENRGYRTA-SVIAL 148  
DB 204 FTEFKSSLSPOSLVDALVQLQ-----GLTYASGIQKVKELFHSKNGARKSAAKILIVI 258  
QY 149 TDGELHEDLFFYSE--REANRSRDGAIVYCVGVND-FNE-TOLARI-----ADSKDHVF 199  
DB 259 TDGQKFRPDLRYRHYIPEAEKA---GIRYALGVGDAREPFTALQELMTTISAPSQDHVF 315

QY 200 PVNDGFOALOGIHSILKSCIEILAEPTICAGESFOVVVNGGFRHARVD 253  
DB 316 KVGK-FVALRSTQRIQEK-----IFALIGTSRSSSSSFQHEMSQEGFSSALSM 364

## RESULT 10

US-08-485-618-53  
Sequence 53, Application US/08485618  
Patent No. 5728533  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
APPLICANT: Van der Vieren, Monica  
TITLE OF INVENTION: No. 5728533e1 Human 2 Integrin Alpha Subunit  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Seear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,618  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32797  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-0448  
TELEFAX: 312-474-6300  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1161 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-485-618-53

Query Match 8.7%; Score 166; DB 1; Length 1161;  
Best Local Similarity 28.2%; Pred. No. 7.6e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYG-GRDLYFLIDKSGSV-LHMHNEIYFVEQALAHKFIISPOLMSEFIVSTRTGTTLMK 94  
DB 144 PECQEQENDIAFLIDGSSSIDQSDPTQMKDFVKALMGQLASTSTSFSLMOYSNLIKTHFT 203  
QY 95 LTEDR-----EQIRQGLEELQKVLPGSDTYMHGFERASEQIYYENRGYRTA-SVIAL 148  
DB 204 FTEFKSSLSPOSLVDALVQLQ-----GLTYASGIQKVKELFHSKNGARKSAAKILIVI 258  
QY 149 TDGELHEDLFFYSE--REANRSRDGAIVYCVGVND-FNE-TOLARI-----ADSKDHVF 199  
DB 259 TDGQKFRPDLRYRHYIPEAEKA---GIRYALGVGDAREPFTALQELMTTISAPSQDHVF 315  
QY 200 PVNDGFOALOGIHSILKSCIEILAEPTICAGESFOVVVNGGFRHARVD 253

Db 316 KVG-N-FVALRSTIQROIQK-----IFAIGTSSRSSSSFOHMSQEGFSSALSMD 364

## RESULT 11

US-08-362-652-53  
; Sequence 53, Application US/08362652  
; Patent No. 5766850  
; GENERAL INFORMATION:  
; APPLICANT: Gallatin, W. Michael  
; APPLICANT: Van der Vieren, Monica  
; TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit  
; NUMBER OF SEQUENCES: 93  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 South Wacker Drive, 6300 Seear Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/362,652  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/173,497  
; FILING DATE: 23-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/286,889  
; FILING DATE: 5-AUG-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams Jr., Joseph A.  
; REGISTRATION NUMBER: 38,659  
; REFERENCE/DOCKET NUMBER: 27866/32391  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; TELEFAX: 312-474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1161 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-362-652-53

Query Match 8.7%; Score 166, DB 1; Length 1161;

Best Local Similarity 28.2%; Pred. No. 7.6e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

Qy 37 PACYG-GFDLYFLIDSGSV-LHHMNEIYFVEQLAHKFTSPQLRMSFIVPSTRTGLTMK 94  
Db 144 PECCGQEMDIAPFLIDGSSSIDQSDFTQMKDFVAKLMQGLASTSTSFSLMQYSNLKTHFT 203  
Qy 95 LTEDR-----EQIRGGLLEIQKVLPGGDTYMHGFEASQIYYENQGYRTA-SVIAL 148  
Db 204 FTEFKSSLSPOSILVDALVQLQ-----GLTYTASGIQKVVLELPHSKNGARKSAKKIILIVI 258  
Qy 149 TDGELHEDLFFYSE--REANRSRLGAIYVCVKD-FNE-TOLARI-----ADSKDHF 199  
Db 259 TDGQKFRDPLEYRHVIPAERA---GIIRYALIGVDAREFTALQELNLTIGSAPSQDHVF 315  
Qy 200 PVNDGFOALGIIHSLKSCIEILAEPSTICAGESFOVVVVGNGFRHARNVD 253  
Db 316 KVG-N-FVALRSTIQROIQK-----IFAIGTSSRSSSSFOHMSQEGFSSALSMD 364

## RESULT 12

US-08-605-672-53  
; Sequence 53, Application US/08605672  
; Patent No. 5817515  
; GENERAL INFORMATION:  
; APPLICANT: Gallatin, W. Michael  
; APPLICANT: Van der Vieren, Monica  
; TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 South Wacker Drive, 6300 Seear Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/605,672  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/173,497  
; FILING DATE: 23-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/286,889  
; FILING DATE: 5-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/362,652  
; FILING DATE: 21-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams Jr., Joseph A.  
; REGISTRATION NUMBER: 38,659  
; REFERENCE/DOCKET NUMBER: 27866/32684  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; TELEFAX: 312-474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1161 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-605-672-53

Query Match 8.7%; Score 166, DB 2; Length 1161;

Best Local Similarity 28.2%; Pred. No. 7.6e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

Qy 37 PACYG-GFDLYFLIDSGSV-LHHMNEIYFVEQLAHKFTSPQLRMSFIVPSTRTGLTMK 94  
Db 144 PECCGQEMDIAPFLIDGSSSIDQSDFTQMKDFVAKLMQGLASTSTSFSLMQYSNLKTHFT 203  
Qy 95 LTEDR-----EQIRGGLLEIQKVLPGGDTYMHGFEASQIYYENQGYRTA-SVIAL 148  
Db 204 FTEFKSSLSPOSILVDALVQLQ-----GLTYTASGIQKVVLELPHSKNGARKSAKKIILIVI 258  
Qy 149 TDGELHEDLFFYSE--REANRSRLGAIYVCVKD-FNE-TOLARI-----ADSKDHF 199  
Db 259 TDGQKFRDPLEYRHVIPAERA---GIIRYALIGVDAREFTALQELNLTIGSAPSQDHVF 315  
Qy 200 PVNDGFOALGIIHSLKSCIEILAEPSTICAGESFOVVVVGNGFRHARNVD 253  
Db 316 KVG-N-FVALRSTIQROIQK-----IFAIGTSSRSSSSFOHMSQEGFSSALSMD 364

## RESULT 13

US-08-482-293A-53  
; Sequence 53, Application US/08482293A



Patent No. 5831029  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Sear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,293A  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1161 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-482-293A-53

Query Match 8.7%; Score 166; DB 2; Length 1161;  
Best Local Similarity 28.2%; Pred. No. 7.6e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYG-GFDLYFLIDKSSV-LHHNNEIYFVEQLAHKFISPOLRMSFIVSTGTITMK 94  
DB 144 PECQOEMDIAPLIDGSSIDQSDFTQMKDFKALMQLASTSTSFSLMOYSNLIKHTFT 203  
QY 95 LTEDR-----EQIRGELBELQKVLPGDPTVMHEGPERASEQIYYENRGYRTA-SVITL 148  
DB 204 FTERKSSISPSQSLVDALVOLQ-----GLTYASGIQKVKELFKNGARKSAAKILIVI 258  
QY 149 TDGELHEDLFYYSR--REANRSRDGAIVYCVGVD-FNE-TOLARI-----ADSKDHF 199  
DB 259 TDGQKFRPRLRYRHYIPAEAKA---GIRYAGVGDAREPPLAQELNTIGSAPSDHVF 315  
QY 200 PVNDGFOLQGIHSLKSCIEILAEPSITCAGESFOVVVRNGRFRHARND 253  
DB 316 KVGK-FVALRSIORIOEK---IFAIGTESRSSSFQHEMSQEGFSSALSMD 364

RESULT 14  
US-08-943-363-53  
Sequence 53, Application US/08943363  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael

APPLICANT: Gallatin, W. Michael  
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Sear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,363  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1161 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-943-363-53

Query Match 8.7%; Score 166; DB 2; Length 1161;  
Best Local Similarity 28.2%; Pred. No. 7.6e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

QY 37 PACYG-GFDLYFLIDKSSV-LHHNNEIYFVEQLAHKFISPOLRMSFIVSTGTITMK 94  
DB 144 PECQOEMDIAPLIDGSSIDQSDFTQMKDFKALMQLASTSTSFSLMOYSNLIKHTFT 203  
QY 95 LTEDR-----EQIRGELBELQKVLPGDPTVMHEGPERASEQIYYENRGYRTA-SVITL 148  
DB 204 FTERKSSISPSQSLVDALVOLQ-----GLTYASGIQKVKELFKNGARKSAAKILIVI 258  
QY 149 TDGELHEDLFYYSR--REANRSRDGAIVYCVGVD-FNE-TOLARI-----ADSKDHF 199  
DB 259 TDGQKFRPRLRYRHYIPAEAKA---GIRYAGVGDAREPPLAQELNTIGSAPSDHVF 315  
QY 200 PVNDGFOLQGIHSLKSCIEILAEPSITCAGESFOVVVRNGRFRHARND 253  
DB 316 KVGK-FVALRSIORIOEK---IFAIGTESRSSSFQHEMSQEGFSSALSMD 364

RESULT 15  
US-09-193-043-53  
Sequence 53, Application US/09193043  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
APPLICANT: Van der Vlieten, Monica

;; TITLE OF INVENTION: No. 6251395e1 Human 2  
;; FILE REFERENCE: 27866/35004  
;; CURRENT APPLICATION NUMBER: US/09/193,043  
;; CURRENT FILING DATE: 1998-11-16  
;; EARLIER APPLICATION NUMBER: 08/173,497  
;; EARLIER FILING DATE: 1993-12-23  
;; EARLIER APPLICATION NUMBER: 08/286,889  
;; EARLIER FILING DATE: 1994-08-05  
;; EARLIER APPLICATION NUMBER: 08/362,652  
;; EARLIER FILING DATE: 1994-12-21  
;; EARLIER APPLICATION NUMBER: 08/343,363  
;; NUMBER OF SEQ ID NOS: 114  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO: 53  
;; LENGTH: 1161  
;; TYPE: prt  
;; ORGANISM: Mus musculus  
US-09-193-043-53

Query Match 8.7%; Score 166; DB 3; Length 1161;

Best Local Similarity 28.2%; Pred. No. 7.6e-09;  
Matches 66; Conservative 42; Mismatches 96; Indels 30; Gaps 12;

OY 37 PACYG-GFDLYFIDKSGSV-LHWNELIYFVEQLAHKFI SPQLMSFIVFSTRGTTLMK 94  
Db 144 PECPQEMDI AFLIDSGSIDQSDFTQMKDFKALMQLASTSTSFSLMQYSNIIKTHFT 203  
OY 95 LTEDR-----EQIQGLEELQKVLBGDPTVMHEGFERASEQIYYENRGYRTA-SVITAI 148  
Db 204 FTEFKSSLSPOSVDALVQLQ----GLTYASGIQKVVKELFHSKNGARKSAKKILIVI 258  
OY 149 TDGELHEDLFPYSE--REANRSRDGAIVYCVGVKD-FNE-TOLARI-----ADSKDHVF 199  
Db 259 TDGQKFRDPLEYRHYIPAEKA---GIIRVAIGVDAREPTALQELNTIGSAPSQDHVF 315  
OY 200 PVNDGFQALQGIHSLKSCIEIIAAEPSTICAGESFOVVVRNGNFRHARNVD 253  
Db 316 KVGN-FVALRSIQRIQEK---IFAIRGTSRSSSSSFQHEMSQEGFSALSMD 364

Search completed: June 21, 2004, 13:46:34  
Job time : 14.8962 secs

Qy 241 VRGNGFRHARVDRVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKKAALQVSMN 300  
Db 241 VRGNGFRHARVDRVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKKAALQVSMN 300  
Qy 301 DGLSFSSSVIITTHCS 318  
Db 301 DGLSFSSSVIITTHCS 318

RESULT 14  
US-10-038-307-24

; Sequence 24, Application US/10038307  
; Publication No. US20030134786A1  
; GENERAL INFORMATION:  
; APPLICANT: James B. ROTTMAN  
; APPLICANT: Theresa L. O'KEEFE  
; APPLICANT: Judith J. HEALEY  
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
; FILE REFERENCE: 7853-253-999  
; CURRENT APPLICATION NUMBER: US/10/038,307  
; CURRENT FILING DATE: 2002-06-28  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-038-307-24

Query Match

Best Local Similarity 100.0%; Score 1649; DB 14; Length 345;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATARRALGIGFQWLSLATTVLICAGGGRREDGPA CYGFPDLYFLIDKSGSVLHNMN 60  
Db 1 MATARRALGIGFQWLSLATTVLICAGGGRREDGPA CYGFPDLYFLIDKSGSVLHNMN 60  
Qy 61 EIIYFVEQLAKHFTSPQLRMSFIVSTRGTTLMKLTEDREQIRQGLEELQVLPBGDTYM 120  
Db 61 EIIYFVEQLAKHFTSPQLRMSFIVSTRGTTLMKLTEDREQIRQGLEELQVLPBGDTYM 120  
Qy 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSRDIGAIYVCYGV 180  
Db 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSRDIGAIYVCYGV 180  
Qy 181 KDFNETQARIADSKDHFVPVNDGFQALQGIHSLKSCIEIIAEPSTICAGESFQV 240  
Db 181 KDFNETQARIADSKDHFVPVNDGFQALQGIHSLKSCIEIIAEPSTICAGESFQV 240  
Qy 241 VRGNGFRHARVDRVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKKAALQVSMN 300  
Db 241 VRGNGFRHARVDRVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKKAALQVSMN 300  
Qy 301 DGLSFSSSVIITTHCS 318  
Db 301 DGLSFSSSVIITTHCS 318

RESULT 15  
US-10-201-292-24

; Sequence 24, Application US/10201292  
; Publication No. US20030144193A1  
; GENERAL INFORMATION:  
; APPLICANT: James B. ROTTMAN  
; APPLICANT: Theresa L. O'KEEFE  
; APPLICANT: Engin OZKANAK  
; APPLICANT: Judith J. HEALEY  
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods  
; FILE REFERENCE: 7853-253-999  
; CURRENT APPLICATION NUMBER: US/10/201,292  
; CURRENT FILING DATE: 2003-02-14  
; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-201-292-24

Query Match  
Best Local Similarity 100.0%; Score 1649; DB 14; Length 345;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATARRALGIGFQWLSLATTVLICAGGGRREDGPA CYGFPDLYFLIDKSGSVLHNMN 60  
Db 1 MATARRALGIGFQWLSLATTVLICAGGGRREDGPA CYGFPDLYFLIDKSGSVLHNMN 60  
Qy 61 EIIYFVEQLAKHFTSPQLRMSFIVSTRGTTLMKLTEDREQIRQGLEELQVLPBGDTYM 120  
Db 61 EIIYFVEQLAKHFTSPQLRMSFIVSTRGTTLMKLTEDREQIRQGLEELQVLPBGDTYM 120  
Qy 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSRDIGAIYVCYGV 180  
Db 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSRDIGAIYVCYGV 180  
Qy 181 KDFNETQARIADSKDHFVPVNDGFQALQGIHSLKSCIEIIAEPSTICAGESFQV 240  
Db 181 KDFNETQARIADSKDHFVPVNDGFQALQGIHSLKSCIEIIAEPSTICAGESFQV 240  
Qy 241 VRGNGFRHARVDRVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKKAALQVSMN 300  
Db 241 VRGNGFRHARVDRVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKKAALQVSMN 300  
Qy 301 DGLSFSSSVIITTHCS 318  
Db 301 DGLSFSSSVIITTHCS 318

Search completed: June 21, 2004, 14:02:12  
Job time : 38.7256 secs

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; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 12
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-753-12
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Query Match      86.2%; Score 1649; DB 10; Length 333;
Best Local Similarity 100.0%; Pred. No. 2,4e-162;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MATERRALGIGFQWLSLATLVLCAGQGRREDGPGACYGFDLYTLDKSGSVLHHMN 60
Db 1 MATERRALGIGFQWLSLATLVLCAGQGRREDGPGACYGFDLYTLDKSGSVLHHMN 60
Qy 61 EIIYFVEQLAHKFIISPOLRMSFIVSTRTGTTLMKLTEDRQIQGLELQVLPBGDTYM 120
Db 61 EIIYFVEQLAHKFIISPOLRMSFIVSTRTGTTLMKLTEDRQIQGLELQVLPBGDTYM 120
Qy 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSDIGAIYVCV 180
Db 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSDIGAIYVCV 180
Qy 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAEPSTTCAGESFOVV 240
Db 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAEPSTTCAGESFOVV 240
Qy 241 VRGNGFRHARNVDRVLCSPKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGKKAALQVSMN 300
Db 241 VRGNGFRHARNVDRVLCSPKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGKKAALQVSMN 300
Qy 301 DGLSFIISSVITTTTCS 318
Db 301 DGLSFIISSVITTTTCS 318
```

```

RESULT 12
US-10-038-307-2
; Sequence 2, Application US/10038307
; Publication No. US20030134786a1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/038,307
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
```

```

; ORGANISM: Homo sapiens
US-10-038-307-2
```

```

Query Match      86.2%; Score 1649; DB 14; Length 333;
Best Local Similarity 100.0%; Pred. No. 2,4e-162;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

Qy 1 MATERRALGIGFQWLSLATLVLCAGQGRREDGPGACYGFDLYTLDKSGSVLHHMN 60
Db 1 MATERRALGIGFQWLSLATLVLCAGQGRREDGPGACYGFDLYTLDKSGSVLHHMN 60
Qy 61 EIIYFVEQLAHKFIISPOLRMSFIVSTRTGTTLMKLTEDRQIQGLELQVLPBGDTYM 120
Db 61 EIIYFVEQLAHKFIISPOLRMSFIVSTRTGTTLMKLTEDRQIQGLELQVLPBGDTYM 120
Qy 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSDIGAIYVCV 180
Db 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSDIGAIYVCV 180
Qy 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAEPSTTCAGESFOVV 240
Db 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAEPSTTCAGESFOVV 240
Qy 241 VRGNGFRHARNVDRVLCSPKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGKKAALQVSMN 300
Db 241 VRGNGFRHARNVDRVLCSPKINDSVTLNEKPFSEVEDTYLLCPAPILKEVGKKAALQVSMN 300
Qy 301 DGLSFIISSVITTTTCS 318
Db 301 DGLSFIISSVITTTTCS 318
```

```

RESULT 13
US-10-201-292-2
; Sequence 2, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-2
```

```

Query Match      86.2%; Score 1649; DB 14; Length 333;
Best Local Similarity 100.0%; Pred. No. 2,4e-162;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy 1 MATERRALGIGFQWLSLATLVLCAGQGRREDGPGACYGFDLYTLDKSGSVLHHMN 60
Db 1 MATERRALGIGFQWLSLATLVLCAGQGRREDGPGACYGFDLYTLDKSGSVLHHMN 60
Qy 61 EIIYFVEQLAHKFIISPOLRMSFIVSTRTGTTLMKLTEDRQIQGLELQVLPBGDTYM 120
Db 61 EIIYFVEQLAHKFIISPOLRMSFIVSTRTGTTLMKLTEDRQIQGLELQVLPBGDTYM 120
Qy 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSDIGAIYVCV 180
Db 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERANRSDIGAIYVCV 180
Qy 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAEPSTTCAGESFOVV 240
Db 181 KDFNETOLARIADSKDHFVPVNDGFQALOGIHSILKSCIEIIAEPSTTCAGESFOVV 240
```

Db 307 SVIITTHCSDGSIILALVLFLLALALALMWFWPLCCTVIKEVPPVVEESEE 362

RESULT 9

US-10-038-307-18

Sequence 18, Application US/10038307

Publication No. US20030134786A1

GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/038,307

CURRENT FILING DATE: 2002-06-26

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 18

LENGTH: 551

TYPE: PRT

ORGANISM: Homo sapiens

US-10-038-307-18

Query Match 86.8%; Score 1661; DB 14; Length 551;

Best Local Similarity 100.0%; Pred. No. 3e-163;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATARRALGIGFQWLSLTLVLICAGGGRREDGDPACVGGFDLYFLIDKSGSVLHHWN 60

Db 1 MATARRALGIGFQWLSLTLVLICAGGGRREDGDPACVGGFDLYFLIDKSGSVLHHWN 60

Qy 61 EIIYVEQOLAHKFI SPOLRMSFI VSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120

Db 61 EIIYVEQOLAHKFI SPOLRMSFI VSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120

Qy 61 EIIYVEQOLAHKFI SPOLRMSFI VSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120

Db 61 EIIYVEQOLAHKFI SPOLRMSFI VSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120

Qy 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERBANRSRDIGAIVYCVGV 180

Db 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERBANRSRDIGAIVYCVGV 180

Qy 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERBANRSRDIGAIVYCVGV 180

Db 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERBANRSRDIGAIVYCVGV 180

Qy 181 KDFNETQIARLADSKDHFVPVNDGFQALOGIHSILKSCIEIIAABSTICAGESFGV 240

Db 181 KDFNETQIARLADSKDHFVPVNDGFQALOGIHSILKSCIEIIAABSTICAGESFGV 240

Qy 241 VRNGFRRARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKKAALQVSMN 300

Db 241 VRNGFRRARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKKAALQVSMN 300

Qy 241 VRNGFRRARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKKAALQVSMN 300

Db 241 VRNGFRRARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKKAALQVSMN 300

Qy 301 DGLSFSSSVIITTHCSDG 320

Db 301 DGLSFSSSVIITTHCSDG 320

RESULT 10

US-10-201-292-18

Sequence 18, Application US/10201292

Publication No. US20030144193A1

GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/201,292

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 36

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 18

LENGTH: 551

TYPE: PRT

ORGANISM: Homo sapiens

US-10-201-292-18

Query Match 86.8%; Score 1661; DB 14; Length 551;

Best Local Similarity 100.0%; Pred. No. 3e-163;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATARRALGIGFQWLSLTLVLICAGGGRREDGDPACVGGFDLYFLIDKSGSVLHHWN 60

Db 1 MATARRALGIGFQWLSLTLVLICAGGGRREDGDPACVGGFDLYFLIDKSGSVLHHWN 60

Qy 61 EIIYVEQOLAHKFI SPOLRMSFI VSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120

Db 61 EIIYVEQOLAHKFI SPOLRMSFI VSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120

Qy 61 EIIYVEQOLAHKFI SPOLRMSFI VSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120

Db 61 EIIYVEQOLAHKFI SPOLRMSFI VSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120

Qy 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERBANRSRDIGAIVYCVGV 180

Db 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERBANRSRDIGAIVYCVGV 180

Qy 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERBANRSRDIGAIVYCVGV 180

Db 121 HEGFERASEQIYYENRQGYRTASVIALTDGELHEDLFFYSERBANRSRDIGAIVYCVGV 180

Qy 181 KDFNETQIARLADSKDHFVPVNDGFQALOGIHSILKSCIEIIAABSTICAGESFGV 240

Db 181 KDFNETQIARLADSKDHFVPVNDGFQALOGIHSILKSCIEIIAABSTICAGESFGV 240

Qy 241 VRNGFRRARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKKAALQVSMN 300

Db 241 VRNGFRRARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAPILKEVGKKAALQVSMN 300

Qy 301 DGLSFSSSVIITTHCSDG 320

Db 301 DGLSFSSSVIITTHCSDG 320

RESULT 11

US-09-796-753-12

Sequence 12, Application US/09796753

Publication No. US20030027998A1

GENERAL INFORMATION:

APPLICANT: McCarthy, Sean A.

TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF

FILE REFERENCE: 7853-227-999

CURRENT APPLICATION NUMBER: US/09/796,753

CURRENT FILING DATE: 2001-03-01

PRIOR APPLICATION NUMBER: 09/183,175

PRIOR FILING DATE: 1998-10-30

PRIOR APPLICATION NUMBER: 09/223,094

PRIOR FILING DATE: 1998-12-30

PRIOR APPLICATION NUMBER: 09/223,546

PRIOR FILING DATE: 1998-12-30

PRIOR APPLICATION NUMBER: 09/224,246

PRIOR FILING DATE: 1998-12-30

PRIOR APPLICATION NUMBER: 09/259,388

PRIOR FILING DATE: 1999-02-26

PRIOR APPLICATION NUMBER: 60/122,458

PRIOR FILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: 09/312,359

PRIOR FILING DATE: 1999-05-14

PRIOR APPLICATION NUMBER: 09/336,536

PRIOR FILING DATE: 1999-06-18

PRIOR APPLICATION NUMBER: 09/342,687

PRIOR FILING DATE: 1999-06-29

PRIOR APPLICATION NUMBER: 09/345,464

PRIOR FILING DATE: 1999-06-30

PRIOR APPLICATION NUMBER: 09/365,164

PRIOR FILING DATE: 1999-07-30

PRIOR APPLICATION NUMBER: 09/399,723

PRIOR FILING DATE: 1999-09-20

PRIOR APPLICATION NUMBER: 09/409,634

PRIOR FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: 09/471,179

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: 09/474,071

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: 09/474,072

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: 09/514,010

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
NAME/KEY: SITE  
LOCATION: (368)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-833-245-620

Query Match 97.7%; Score 1870; DB 11; Length 403;  
Best Local Similarity 96.1%; Pred. No. 3.5e-185;  
Matches 360; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATARRALGIGFQWLSLAVLILICAGGGRREDGPAICYGFDLYFLIDKSGSVLHNNIYFVEQ 60  
DB 1 MATARRALGIGFQWLSLAVLILICAGGGRREDGPAICYGFDLYFLIDKSGSVLHNNIYFVEQ 60  
QY 61 EIIYFVEQLANKFISPOLRMSFIVSTGTTLTKLTEDREOIRQGLELQVLPQGDYTM 120  
DB 61 EIIYFVEQLANKFISPOLRMSFIVSTGTTLTKLTEDREOIRQGLELQVLPQGDYTM 120  
QY 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYVCVGV 180  
DB 121 HEGFERASEQIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYVCVGV 180  
QY 181 KDFNETOLARIADSKDHFVPVNDGFQALQGIHSLKSCIEILAAEPSTICAGESPQV 240  
DB 181 KDFNETOLARIADSKDHFVPVNDGFQALQGIHSLKSCIEILAAEPSTICAGESPQV 240  
QY 241 VRGNGFRHARVNDVLCSPKINDSVTLNEKPSVEDTYLCPAPILKEVGKALQVSMN 300  
DB 241 VRGNGFRHARVNDVLCSPKINDSVTLNEKPSVEDTYLCPAPILKEVGKALQVSMN 300  
QY 301 DGLSFISGVITTHGSDGSLAIALILFLLALALMMFWPLCCTVVIKEVPPPAE 360  
DB 301 DGLSFISGVITTHGSDGSLAIALILFLLALALMMFWPLCCTVVIKEVPPPAE 360  
QY 361 ESE 363  
DB 361 ESE 363

RESULT 7  
US-09-918-715-194  
Sequence 194, Application US/09918715  
Publication No. US20030017157A1  
GENERAL INFORMATION:  
APPLICANT: Brad St. Croix  
APPLICANT: Bert Vogelstein  
APPLICANT: Kenneth Kinzler  
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
FILE REFERENCE: 1107.00134  
CURRENT APPLICATION NUMBER: US/09/918,715  
CURRENT FILING DATE: 2001-08-01  
PRIOR APPLICATION NUMBER: 60/222,599  
PRIOR FILING DATE: 2000-08-02  
PRIOR APPLICATION NUMBER: 60/224,360  
PRIOR FILING DATE: 2000-08-11  
PRIOR APPLICATION NUMBER: 60/282,850  
PRIOR FILING DATE: 2000-04-11  
NUMBER OF SEQ ID NOS: 358  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 194  
LENGTH: 562  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-918-715-194

Query Match 93.7%; Score 1793; DB 12; Length 562;  
Best Local Similarity 96.1%; Pred. No. 5.8e-177;  
Matches 342; Conservative 6; Mismatches 8; Indels 0; Gaps 0;  
QY 9 LGIGFQWLSLAVLILICAGGGRREDGPAICYGFDLYFLIDKSGSVLHNNIYFVEQ 68  
DB 7 LGIGFQWLSLAVLILICAGGGRREDGPAICYGFDLYFLIDKSGSVLHNNIYFVEQ 66

QY 69 LAHKFISPOLRMSFIVSTGTTLTKLTEDREOIRQGLELQVLPQGDYTMHEGFERAS 128  
DB 67 LAHKFISPOLRMSFIVSTGTTLTKLTEDREOIRQGLELQVLPQGDYTMHEGFERAS 126  
QY 129 EOIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYVCVGVDFNETOL 188  
DB 127 EOIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYVCVGVDFNETOL 186  
QY 189 ARIADSKDHFVPVNDGFQALQGIHSLKSCIEILAAEPSTICAGESFOVVRGNGFRH 248  
DB 187 ARIADSKDHFVPVNDGFQALQGIHSLKSCIEILAAEPSTICAGESFOVVRGNGFRH 246  
QY 249 ARVNDVRLCSFKINDSVTLNEKPSVEDTYLCPAPILKEVGKALQVSMNGLSFIS 308  
DB 247 ARVNDVRLCSFKINDSVTLNEKPSVEDTYLCPAPILKEVGKALQVSMNGLSFIS 306  
QY 309 SVITTHGSDGSLAIALILFLLALALMMFWPLCCTVVIKEVPPPAESEE 364  
DB 307 SVITTHGSDGSLAIALILFLLALALMMFWPLCCTVVIKEVPPPAESEE 362

RESULT 8  
US-09-918-715-301  
Sequence 301, Application US/09918715  
Publication No. US20030017157A1  
GENERAL INFORMATION:  
APPLICANT: Brad St. Croix  
APPLICANT: Bert Vogelstein  
APPLICANT: Kenneth Kinzler  
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
FILE REFERENCE: 1107.00134  
CURRENT APPLICATION NUMBER: US/09/918,715  
CURRENT FILING DATE: 2001-08-01  
PRIOR APPLICATION NUMBER: 60/222,599  
PRIOR FILING DATE: 2000-08-02  
PRIOR APPLICATION NUMBER: 60/224,360  
PRIOR FILING DATE: 2000-08-11  
PRIOR APPLICATION NUMBER: 60/282,850  
PRIOR FILING DATE: 2000-04-11  
NUMBER OF SEQ ID NOS: 358  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 301  
LENGTH: 562  
TYPE: PRT  
ORGANISM: Mouse  
US-09-918-715-301

Query Match 93.7%; Score 1793; DB 12; Length 562;  
Best Local Similarity 96.1%; Pred. No. 5.8e-177;  
Matches 342; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 9 LGIGFQWLSLAVLILICAGGGRREDGPAICYGFDLYFLIDKSGSVLHNNIYFVEQ 68  
DB 7 LGIGFQWLSLAVLILICAGGGRREDGPAICYGFDLYFLIDKSGSVLHNNIYFVEQ 66  
QY 69 LAHKFISPOLRMSFIVSTGTTLTKLTEDREOIRQGLELQVLPQGDYTMHEGFERAS 128  
DB 67 LAHKFISPOLRMSFIVSTGTTLTKLTEDREOIRQGLELQVLPQGDYTMHEGFERAS 126  
QY 129 EOIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYVCVGVDFNETOL 188  
DB 127 EOIYENRQGYRTASVIALTDGELHEDLFFYSERANRSDGAIYVCVGVDFNETOL 186  
QY 189 ARIADSKDHFVPVNDGFQALQGIHSLKSCIEILAAEPSTICAGESFOVVRGNGFRH 248  
DB 187 ARIADSKDHFVPVNDGFQALQGIHSLKSCIEILAAEPSTICAGESFOVVRGNGFRH 246  
QY 249 ARVNDVRLCSFKINDSVTLNEKPSVEDTYLCPAPILKEVGKALQVSMNGLSFIS 308  
DB 247 ARVNDVRLCSFKINDSVTLNEKPSVEDTYLCPAPILKEVGKALQVSMNGLSFIS 306  
QY 309 SVITTHGSDGSLAIALILFLLALALMMFWPLCCTVVIKEVPPPAESEE 364  
DB 307 SVITTHGSDGSLAIALILFLLALALMMFWPLCCTVVIKEVPPPAESEE 362

```
RESULT 4
US-10-408-765A-1823
; Sequence 1823, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Choeh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Marnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FASTSeq for Windows Version 4.0
; SEQ ID NO: 1823
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1823

Query Match      99.0%; Score 1894; DB 16; Length 564;
Best Local Similarity 100.0%; Pred. No. 1.9e-187;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MATARRALGIGFQWLSLATLVLLICAGQGGRRDEGGPACYGFDLYFLIDKSGSVLHHMN 60
DB      1 MATARRALGIGFQWLSLATLVLLICAGQGGRRDEGGPACYGFDLYFLIDKSGSVLHHMN 60
QY      61 EIIYFVEQLAHKFIISPOLRMSFIYFSTRGTTLMKLTEDREQIRQGLELOVLPQGGDTYM 120
DB      61 EIIYFVEQLAHKFIISPOLRMSFIYFSTRGTTLMKLTEDREQIRQGLELOVLPQGGDTYM 120
QY      121 HEGFERASEQIYYENRQGYRTASVITIALTDGELHEDLFFYSERERANSRDIGAIYVCYGV 180
DB      121 HEGFERASEQIYYENRQGYRTASVITIALTDGELHEDLFFYSERERANSRDIGAIYVCYGV 180
QY      181 KDFNETQLARIADSKDHFVPVNDGFQALQGIHISILKSCIEIIAABSTTCAGBSFQV 240
DB      181 KDFNETQLARIADSKDHFVPVNDGFQALQGIHISILKSCIEIIAABSTTCAGBSFQV 240
QY      241 VRGNGFRRARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAFLKEVGKKAALQVSMN 300
DB      241 VRGNGFRRARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAFLKEVGKKAALQVSMN 300
QY      301 DGLSFSSSVITTTTHCSGDSILAIALILFLALLALMLMFWPLCCTVIIKEVPPPPAE 360
DB      301 DGLSFSSSVITTTTHCSGDSILAIALILFLALLALMLMFWPLCCTVIIKEVPPPPAE 360
QY      361 ESEE 364
DB      361 ESEE 364

RESULT 5
US-09-833-245-621
; Sequence 621, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
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; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 621
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-621

Query Match      98.7%; Score 1889; DB 11; Length 403;
Best Local Similarity 100.0%; Pred. No. 3.7e-187;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MATARRALGIGFQWLSLATLVLLICAGQGGRRDEGGPACYGFDLYFLIDKSGSVLHHMN 60
DB      1 MATARRALGIGFQWLSLATLVLLICAGQGGRRDEGGPACYGFDLYFLIDKSGSVLHHMN 60
QY      61 EIIYFVEQLAHKFIISPOLRMSFIYFSTRGTTLMKLTEDREQIRQGLELOVLPQGGDTYM 120
DB      61 EIIYFVEQLAHKFIISPOLRMSFIYFSTRGTTLMKLTEDREQIRQGLELOVLPQGGDTYM 120
QY      121 HEGFERASEQIYYENRQGYRTASVITIALTDGELHEDLFFYSERERANSRDIGAIYVCYGV 180
DB      121 HEGFERASEQIYYENRQGYRTASVITIALTDGELHEDLFFYSERERANSRDIGAIYVCYGV 180
QY      181 KDFNETQLARIADSKDHFVPVNDGFQALQGIHISILKSCIEIIAABSTTCAGBSFQV 240
DB      181 KDFNETQLARIADSKDHFVPVNDGFQALQGIHISILKSCIEIIAABSTTCAGBSFQV 240
QY      241 VRGNGFRRARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAFLKEVGKKAALQVSMN 300
DB      241 VRGNGFRRARNDVRLCSFKINDSVTLNEKPSVEDTYLLCPAFLKEVGKKAALQVSMN 300
QY      301 DGLSFSSSVITTTTHCSGDSILAIALILFLALLALMLMFWPLCCTVIIKEVPPPPAE 360
DB      301 DGLSFSSSVITTTTHCSGDSILAIALILFLALLALMLMFWPLCCTVIIKEVPPPPAE 360
QY      361 ESE 363
DB      361 ESE 363

RESULT 6
US-09-833-245-620
; Sequence 620, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 620
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (175)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (320)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (331)
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Qy 121 HEGFERASEQIYENROGYRTASVIALTDGELHEDLFYSEERANRSDIGAIVYCVG 180  
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Db 121 HEGFERASEQIYENROGYRTASVIALTDGELHEDLFYSEERANRSDIGAIVYCVG 180  
Qy 181 KDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCIEIIAEPSTICAGESFOV 240  
|  
Db 181 KDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCIEIIAEPSTICAGESFOV 240  
Qy 241 VRGNGFRARAVDRVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300  
|  
Db 241 VRGNGFRARAVDRVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300  
Qy 301 DGLSFSSSVIITTHCSGDSIIAIALILFLALALALMMFWPLCCTVITKEVPPPAE 360  
|  
Db 301 DGLSFSSSVIITTHCSGDSIIAIALILFLALALALMMFWPLCCTVITKEVPPPAE 360  
Qy 361 ESEE 364  
|  
Db 361 ESEE 364

## RESULT 2

US-09-918-715-232  
; Sequence 232, Application US/09918715  
; Publication No. US20030017157A1  
; GENERAL INFORMATION:  
; APPLICANT: Brad St. Croix  
; APPLICANT: Bert Vogelstein  
; APPLICANT: Kenneth Kinzler  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00134  
; CURRENT APPLICATION NUMBER: US/09/918,715  
; CURRENT FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/222,599  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR APPLICATION NUMBER: 60/224,360  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 232  
; LENGTH: 564  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-918-715-232

Query Match Best Local Similarity 100.0%; Score 1894; DB 12; Length 564;

Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGCPACYGFDLYTLDKSGSVLHHMN 60  
|  
Db 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGCPACYGFDLYTLDKSGSVLHHMN 60  
Qy 61 EIIYFVEQLAKHFTSPQLRMSFIVSTRGTMLKLTEDREQIRQGLEBLQVLPFGDPTM 120  
|  
Db 61 EIIYFVEQLAKHFTSPQLRMSFIVSTRGTMLKLTEDREQIRQGLEBLQVLPFGDPTM 120  
Qy 121 HEGFERASEQIYENROGYRTASVIALTDGELHEDLFYSEERANRSDIGAIVYCVG 180  
|  
Db 121 HEGFERASEQIYENROGYRTASVIALTDGELHEDLFYSEERANRSDIGAIVYCVG 180  
Qy 181 KDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCIEIIAEPSTICAGESFOV 240  
|  
Db 181 KDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCIEIIAEPSTICAGESFOV 240  
Qy 241 VRGNGFRARAVDRVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300  
|  
Db 241 VRGNGFRARAVDRVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300  
Qy 301 DGLSFSSSVIITTHCSGDSIIAIALILFLALALALMMFWPLCCTVITKEVPPPAE 360  
|  
Db 301 DGLSFSSSVIITTHCSGDSIIAIALILFLALALALMMFWPLCCTVITKEVPPPAE 360

Db 301 DGLSFSSSVIITTHCSGDSIIAIALILFLALALALMMFWPLCCTVITKEVPPPAE 360  
|  
Qy 361 ESEE 364  
|  
Db 361 ESEE 364

## RESULT 3

US-10-301-822-199  
; Sequence 199, Application US/10301822  
; Publication No. US20030148410A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Berger, Allison  
; APPLICANT: Guillemette, Tracy L.  
; APPLICANT: Kamatkar, Shubhangi  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Monahan, John E.  
; APPLICANT: Thibodeau, Stephen N.  
; APPLICANT: BURGART, Lawrence J.  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; FILE REFERENCE: MEM01-029P2RMM  
; CURRENT APPLICATION NUMBER: US/10/301,822  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 60/339,971  
; PRIOR FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: US 60/361,978  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 60/381,988  
; PRIOR FILING DATE: 2002-05-20  
; NUMBER OF SEQ ID NOS: 228  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 199  
; LENGTH: 564  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-301-822-199

Query Match Best Local Similarity 100.0%; Score 1894; DB 14; Length 564;  
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGCPACYGFDLYTLDKSGSVLHHMN 60  
|  
Db 1 MATERRALGIGFQWLSLATLVLCAGGGRREDGCPACYGFDLYTLDKSGSVLHHMN 60  
Qy 61 EIIYFVEQLAKHFTSPQLRMSFIVSTRGTMLKLTEDREQIRQGLEBLQVLPFGDPTM 120  
|  
Db 61 EIIYFVEQLAKHFTSPQLRMSFIVSTRGTMLKLTEDREQIRQGLEBLQVLPFGDPTM 120  
Qy 121 HEGFERASEQIYENROGYRTASVIALTDGELHEDLFYSEERANRSDIGAIVYCVG 180  
|  
Db 121 HEGFERASEQIYENROGYRTASVIALTDGELHEDLFYSEERANRSDIGAIVYCVG 180  
Qy 181 KDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCIEIIAEPSTICAGESFOV 240  
|  
Db 181 KDFNETOLARIADSKDHVPVNDGFQALOGIHSILKSCIEIIAEPSTICAGESFOV 240  
Qy 241 VRGNGFRARAVDRVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300  
|  
Db 241 VRGNGFRARAVDRVLCSPKINDSVTLNEKPSVEDTYLLCPAPILKEVGKALQVSMN 300  
Qy 301 DGLSFSSSVIITTHCSGDSIIAIALILFLALALALMMFWPLCCTVITKEVPPPAE 360  
|  
Db 301 DGLSFSSSVIITTHCSGDSIIAIALILFLALALALMMFWPLCCTVITKEVPPPAE 360  
Qy 361 ESEE 364  
|  
Db 361 ESEE 364

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 21, 2004, 13:44:26 ; Search time 36.7256 Seconds  
(without alignments)  
2828.859 Million cell updates/sec

Title: US-09-970-076-2

Perfect score: 1914  
Sequence: 1 MATERRALGIGFQWLSLAT.....VILKEVPPPESEENKIK 368

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA.\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1894	99.0	564	US-09-918-715-187	Sequence 187, App
2	1894	99.0	564	US-09-918-715-232	Sequence 232, App
3	1894	99.0	564	US-10-301-822-199	Sequence 199, App
4	1894	99.0	564	US-10-408-765A-1823	Sequence 1823, App
5	1889	98.7	403	US-09-833-245-621	Sequence 621, App
6	1870	97.7	403	US-09-833-245-620	Sequence 620, App
7	1793	93.7	562	US-09-918-715-194	Sequence 194, App
8	1793	93.7	562	US-09-918-715-301	Sequence 301, App
9	1661	86.8	551	US-10-038-307-18	Sequence 18, App1
10	1661	86.8	551	US-10-201-292-18	Sequence 18, App1
11	1649	86.2	333	US-09-796-753-12	Sequence 12, App1
12	1649	86.2	333	US-10-038-307-2	Sequence 2, App1
13	1649	86.2	333	US-10-201-292-2	Sequence 2, App1
14	1649	86.2	345	US-10-038-307-24	Sequence 24, App1
15	1649	86.2	345	US-10-201-292-24	Sequence 24, App1

16	1649	86.2	564	US-10-038-307-20	Sequence 20, App1
17	1649	86.2	564	US-10-201-292-20	Sequence 20, App1
18	1636	85.5	328	US-10-038-307-26	Sequence 26, App1
19	1636	85.5	328	US-10-201-292-26	Sequence 26, App1
20	1634.5	85.4	342	US-10-038-307-22	Sequence 22, App1
21	1634.5	85.4	342	US-10-201-292-22	Sequence 22, App1
22	1629	85.1	543	US-10-038-307-14	Sequence 14, App1
23	1629	85.1	543	US-10-038-307-16	Sequence 16, App1
24	1629	85.1	543	US-10-201-292-14	Sequence 14, App1
25	1629	85.1	543	US-10-201-292-16	Sequence 16, App1
26	1619	84.6	543	US-10-038-307-10	Sequence 10, App1
27	1619	84.6	543	US-10-201-292-10	Sequence 10, App1
28	1548	80.9	529	US-10-201-292-36	Sequence 36, App1
29	1488	77.7	534	US-10-038-307-12	Sequence 12, App1
30	1488	77.7	534	US-10-201-292-12	Sequence 12, App1
31	1434.5	74.9	504	US-10-201-292-34	Sequence 34, App1
32	1307	68.3	479	US-10-201-292-32	Sequence 32, App1
33	1193	62.3	460	US-10-201-292-28	Sequence 28, App1
34	1183	61.8	460	US-10-201-292-30	Sequence 30, App1
35	962.5	50.3	488	US-10-368-087-16	Sequence 16, App1
36	962.5	50.3	488	US-10-104-047-2639	Sequence 2639, App
37	957.5	50.0	488	US-09-796-753-52	Sequence 52, App1
38	957.5	50.0	488	US-10-038-307-6	Sequence 6, App1
39	957.5	50.0	488	US-10-201-292-6	Sequence 6, App1
40	938.5	49.0	587	US-09-764-870-312	Sequence 312, App
41	938.5	49.0	587	US-09-764-875-968	Sequence 968, App
42	938.5	49.0	587	US-10-125-540-312	Sequence 312, App
43	936.5	48.9	487	US-09-796-753-54	Sequence 54, App1
44	936.5	48.9	487	US-10-038-307-8	Sequence 8, App1
45	936.5	48.9	487	US-10-201-292-8	Sequence 8, App1

ALIGNMENTS

RESULT 1  
US-09-918-715-187  
; Sequence 187, Application US/09918715  
; Publication No. US20030017157A1  
; GENERAL INFORMATION:  
; APPLICANT: Brad St. Croix  
; APPLICANT: Beat Vogelstein  
; TITLE OF INVENTION: KENNETH KINZLER  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00134  
; CURRENT APPLICATION NUMBER: US/09/918,715  
; CURRENT FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/222,599  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR APPLICATION NUMBER: 60/224,360  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 187  
; LENGTH: 564  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-918-715-187  
Query Match 99.0%; Score 1894; DB 12; Length 564;  
Best Local Similarity 100.0%; Pred. No. 1.9e-187;  
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MATERRALGIGFQWLSLATVILICAGGGRREDGACGCFDLYFTLDKSGSVLAHNN 60  
DB 1 MATERRALGIGFQWLSLATVILICAGGGRREDGACGCFDLYFTLDKSGSVLAHNN 60  
QY 61 EIVYFVEQLAKHFTSPQRMSEFVSTGTMLMTLTEREQIRQGLEQLVPCGGDTYM 120  
DB 61 EIVYFVEQLAKHFTSPQRMSEFVSTGTMLMTLTEREQIRQGLEQLVPCGGDTYM 120

GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 22, 2004, 01:18:40 ; Search time 80.151 Seconds

(without alignments)  
2547.963 Million cell updates/sec

Title: US-09-970-076-2

Sequence: 1 MATERRALGIGFQWLSLAT.....VIVEKPPPAESENKIK 368

## Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -SPART=1 -END=1 -MATRIX=blowm62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=prco -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US0970076@cgn2\_1\_148@runat\_21062004\_125531\_8763 -NCPU=6 -ICPU=3  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:

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3:	/cgn2_6/ptodata/2/ina/6A.COMB.seq:*
4:	/cgn2_6/ptodata/2/ina/6B.COMB.seq:*
5:	/cgn2_6/ptodata/2/ina/PTUS.COMB.seq:*
6:	/cgn2_6/ptodata/2/ina/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1649	86.2	2459	4	US-09-833-381-998 Sequence 998, App
2	1592	72.7	1609	4	US-09-620-312D-8 Sequence 8, Appl
3	166	8.7	3519	1	US-08-286-889-45 Sequence 45, Appl
4	166	8.7	3519	1	US-08-485-618-45 Sequence 45, Appl
5	166	8.7	3519	1	US-08-362-652-45 Sequence 45, Appl
6	166	8.7	3519	1	US-08-605-672-45 Sequence 45, Appl
7	166	8.7	3519	2	US-08-482-293A-45 Sequence 45, Appl
8	166	8.7	3519	2	US-08-943-363-45 Sequence 45, Appl
9	166	8.7	3519	3	US-09-193-043-45 Sequence 45, Appl
10	166	8.7	3519	4	US-09-688-307A-45 Sequence 45, Appl
11	166	8.7	3519	4	US-09-350-259-45 Sequence 45, Appl
12	166	8.7	3803	1	US-08-485-618-52 Sequence 52, Appl

13	166	8.7	3803	1	US-08-362-652-52 Sequence 52, Appl
14	166	8.7	3803	1	US-08-605-672-52 Sequence 52, Appl
15	166	8.7	3803	2	US-08-482-293A-52 Sequence 52, Appl
16	166	8.7	3803	2	US-08-943-363-52 Sequence 52, Appl
17	166	8.7	3803	3	US-09-193-043-52 Sequence 52, Appl
18	166	8.7	3803	4	US-09-688-307A-52 Sequence 52, Appl
19	166	8.7	3803	4	US-09-350-259-52 Sequence 52, Appl
20	159.5	8.3	2499	1	US-08-485-618-96 Sequence 96, Appl
21	159.5	8.3	2499	1	US-08-605-672-96 Sequence 96, Appl
22	159.5	8.3	2499	2	US-08-482-293A-96 Sequence 96, Appl
23	159.5	8.3	2499	2	US-08-943-363-96 Sequence 96, Appl
24	159.5	8.3	2499	3	US-09-193-043-96 Sequence 96, Appl
25	159.5	8.3	2499	4	US-09-688-307A-96 Sequence 96, Appl
26	159.5	8.3	2499	4	US-09-350-259-96 Sequence 96, Appl
27	159.5	8.3	3528	1	US-08-286-889-36 Sequence 36, Appl
28	159.5	8.3	3528	1	US-08-485-618-36 Sequence 36, Appl
29	159.5	8.3	3528	1	US-08-362-652-36 Sequence 36, Appl
30	159.5	8.3	3528	1	US-08-605-672-36 Sequence 36, Appl
31	159.5	8.3	3528	2	US-08-482-293A-36 Sequence 36, Appl
32	159.5	8.3	3528	2	US-08-943-363-36 Sequence 36, Appl
33	159.5	8.3	3528	3	US-09-193-043-36 Sequence 36, Appl
34	159.5	8.3	3528	4	US-09-688-307A-36 Sequence 36, Appl
35	159.5	8.3	3528	4	US-09-350-259-36 Sequence 36, Appl
36	159.5	8.3	3597	1	US-08-485-618-54 Sequence 54, Appl
37	159.5	8.3	3597	1	US-08-362-652-54 Sequence 54, Appl
38	159.5	8.3	3597	2	US-08-605-672-54 Sequence 54, Appl
39	159.5	8.3	3597	2	US-08-482-293A-54 Sequence 54, Appl
40	159.5	8.3	3597	2	US-08-943-363-54 Sequence 54, Appl
41	159.5	8.3	3597	3	US-09-193-043-54 Sequence 54, Appl
42	159.5	8.3	3597	4	US-09-688-307A-54 Sequence 54, Appl
43	159.5	8.3	3597	4	US-09-350-259-54 Sequence 54, Appl
44	159.5	8.3	3726	1	US-08-173-497-1 Sequence 1, Appl
45	159.5	8.3	3726	1	US-08-286-889-1 Sequence 1, Appl

## ALIGNMENTS

RESULT 1

US-09-833-381-998 Application US/09833381

Patent No. 6672186

GENERAL INFORMATION:

APPLICANT: Robison, Keith E.

TITLE OF INVENTION: NO. 6672186el Nucleic Acid and Protein Homologs

FILE REFERENCE: 5800-119

CURRENT FILING DATE: 2001-04-11

PRIOR APPLICATION NUMBER: 09/516,448

PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 2050

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 998

LENGTH: 2459

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE: NAME/KEY: misc\_feature

LOCATION: (1) ... (2459)

OTHER INFORMATION: n = A,T,C or G

US-09-833-381-998

Alignment Scores:

Pred. No.: 6.95e-194

Score: 1649.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 86.15%

Length: 2459

Matches: 318

Conservative: 0

Mismatch: 0

Indels: 0

Gaps: 0

US-09-970-076-2 (1-368) x US-09-833-381-998 (1-2459)

2/29/00 PD

9/833382

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Db      412 ATGGCAGCGGCGAGCGAGAGCCCTCGGACATCGGCTTCCAGTGGCTCTTTGGCCACT 471
Qy      21 LeuValLeuIleCysAlaGlyGlnGlyValArgArgIleuAspGlyValProAlaCysPheTyr 40
Db      472 CTGGGCTCATCTGGCCGGGAGAGGGGAGCGAGGGAGAGTGGGGGCTCCAGCCTGGCTAC 531
Qy      41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTyrAsn 60
Db      532 GCGCGATTGACCTGTACTTCACTTTTGGACAATCAGAGAGTGTCTGCACACATCGGAT 591
Qy      61 GluIleTyrTyrPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMet 80
Db      592 GAAATCTATTACTTGTGTGAAACAGTTGGCTCCAAATTCATCAGGCCACAGTTGGAGATG 651
Qy      81 SerPheIleValPheSerThrArgGlyThrThrIleuMetLysLeuThrGluAspArgGlu 100
Db      652 TCTTTATTGTTTCTTCCACCGAGGAAACAACCTTAAAGAACTGACAGAAAGACAGAGAA 711
Qy      101 GlnIleArgGlnGlyLeuGlnGlnGlnIleValLeuProGlyGlyAspThrTyrMet 120
Db      712 CAAATCCCTCAAGGCTTGAGAGAACTCCAGAAAGTTCTGCCAGAGAGAGACACTTACATG 771
Qy      121 HisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAspArgGlnGlyTyrArg 140
Db      772 CATGAAAGATTGTGAAGGGCCAGTGAAGCATTTTATTATGAAACAGACAAAGGGTACAGG 831
Qy      141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisIleGluAspLeuPhePheTyr 160
Db      832 ACAGCCAGCGTCATCATTTGCTTGTGACTGAGAGAACTCCAAAGATCTCTTTTCTAT 891
Qy      161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValTyrCysValGlyVal 180
Db      892 TCAGAGAGGAGGCGCAATAGCTCGAGATCTTGGTGCAATTGTTTACGTGGTGATG 951
Qy      181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
Db      952 AAAGATTTCAATGAGACACAGCTGGCCCGGATGGCGGACAGTAAGATCATGTGTTTCC 1011
Qy      201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220
Db      1012 GTGAATGAGGCTTTCAGGCTCTGCAAGGCAATCACTCAATTTTAAAGAGCTCGC 1071
Qy      221 IleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGlySerPheGlnValVal 240
Db      1072 ATCGAAATTTCTTAGAGCTGGAACCAATCCACCAATGTGCAAGAGAGTCACTTCAAGTTTC 1111
Qy      241 ValArgGlyAsnGlyPheArgHisAlaIleArgAsnValAspArgValLeuCysSerPheLys 260
Db      1132 GTGAGAGGAAACGGCTTCCGACATGCCCGCAACGTGACAGGCTCTCTGCAAGCTTCAAG 1191
Qy      261 IleAsnAspSerValThrLeuAsnGlnLysProPheSerValGluAspThrTyrIleuLeu 280
Db      1192 ATCAATGATCGGTACACTCAATAGAAAGCCCTTTCTGTGAGAAAGATCACTTATTACTG 1251
Qy      281 CysProAlaProIleLeuLysGlnValGlyMetLysAlaAlaLeuGlnValSerMetAsn 300
Db      1252 TGTCCAGGCGCTATTTAAAGAGAGTTGGCAATGAAAGCTGCACCTCCAGTACAGATGAA 1311
Qy      301 AspGlyLeuSerPheIleSerSerSerValIleIleThrThrHisCysSer 318
Db      1312 GATGCGCTCTCTTTATCTCCAGTTCTGTCAATCATCACACACACACTGTAGC 1365

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## RESULT 2

US-09-620-312D-8

Sequence 8, Application US/09620312D

Patent No. 6569662

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Asundi, Vinod

APPLICANT: Zhang, Jie

APPLICANT: Ren, Feiyan

APPLICANT: Chen, Rui-hong

```

APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghaast
APPLICANT: Drmanac, Radoye T.
TITLE OF INVENTION: No. 656962e1 Nucleic Acids and
FILE REFERENCE: 784CIP28
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc_Fl_genes Version 1.0
SEQ ID NO 8
LENGTH: 1609
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (309)..(1202)
US-09-620-312D-8

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## Alignment Scores:

Pred. No.:	2,53e-162	Length:	1609
Score:	1392.00	Matches:	267
Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	99.26%	Mismatches:	0
Query Match:	72.73%	Indels:	0
DB:	4	Gaps:	0

US-09-970-076-2 (1-368) x US-09-620-312D-8 (1-1609)

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Qy      1 MetAlaThrAlaGluArgAlaLeuGlyIleGlyPheGlnTyrLeuSerLeuAlaThr 20
Db      309 ATGGCAGCGGCGAGCGAGAGCCCTCGGATCGGCTTCCAGTGGCTCTTTGGCCACT 368
Qy      21 LeuValLeuIleCysAlaGlyGlnGlyValArgArgIleuAspGlyValProAlaCysTyr 40
Db      369 CTGGGCTCATCTGGCCGGGAGAGGGGAGCGAGGAGAGTGGGGGTCCAGCCTGGCTAC 428
Qy      41 GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTyrAsn 60
Db      429 GCGCGATTGACCTGTACTTCACTTTTGGACAATCAGAGAGTGTCTGCACACATCGGAT 488
Qy      61 GluIleTyrTyrPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMet 80
Db      489 GAAATCTATTACTTGTGGAACAGTTGGCTCACAAATTCATCAGCCACAGTTGAGAATG 548
Qy      81 SerPheIleValPheSerThrArgGlyThrThrIleuMetLysLeuThrGluAspArgGlu 100
Db      549 TCTTTATTGTTTCTTCCACCGAGGAAACAACCTTAAATGAACTGACAGAAAGACAGAGAA 608
Qy      101 GlnIleArgGlnGlyLeuGlnGlnGlnIleValLeuProGlyGlyAspThrTyrMet 120
Db      609 CAAATCCCTCAAGGCTTGAGAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTACATG 668
Qy      121 HisGluGlyPheGluArgAlaSerGluGlnIleTyrTyrGluAspArgGlnGlyTyrArg 140
Db      669 CATGAAGATTGTGAAGGGCGAGTGAAGCATTTTATATGAAACAGACAAAGGGTACAGG 728
Qy      141 ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisIleGluAspLeuPhePheTyr 160
Db      729 ACAGCCAGCGTCATCATTTGCTTGTGACTGAGAGAACTCCAAAGATCTCTTTTCTAT 788

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QY 161 SerGIuArgGluAlaAsnArgSerArgPheLeuGlyAlaIleValTyrCyValGlyVal 180  
 DB 789 TCAGAGAGGAGGCGCTATAGCTCTGAGATCTTGCTGCAATTGTTACTGCTGTGTG 848  
 QY 181 LysAspPheAsnGlyThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200  
 DB 849 AAAGATTTCATGAGACACACAGCTGGCCCGGATTCGAGACAGATCATGTGTTCC 908  
 QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220  
 DB 909 GGAATGACGGCTTTCAGGCTCTGCAAGGCAATCATCTCAATTGGAAGAGTCCTGC 968  
 QY 221 IleguIleLeuAlaAlaGluProSerThrIleCysAlaGlyGlySerPheGlnVal 240  
 DB 969 ATCGAATTCTGACAGCTGACCATTCACCATTTGTGCGAGAGATCATTTCAAGTTGTC 1028  
 QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260  
 DB 1029 GTGAGAGGAAACGGCTTCGACATGCCCAACGTGACAGGCTCCTGCGAGCTTCAAG 1088  
 QY 261 IleAsnAspSerValThrLeuAsnGlu 269  
 DB 1089 ATCAATGACTCGTCACTCACTCAGTAA 1115

## RESULT 3

US-08-286-889-45  
 ; Sequence 45, Application US/08286889  
 ; Patent No. 5470953  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gallatin, W. Mich  
 ; APPLICANT: Van der Vieren, Monica  
 ; TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit  
 ; NUMBER OF SEQUENCES: 51  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 ; STREET: 233 South Wacker Drive, 6300 Sear Tower  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: United States  
 ; ZIP: 60606-6402  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/286,889  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/173,497  
 ; FILING DATE: 23-DEC-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Williams Jr., Joseph A.  
 ; REGISTRATION NUMBER: P38,659  
 ; REFERENCE/DOCKET NUMBER: 27866/32168  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312-474-6300  
 ; TELEFAX: 312-474-0448  
 ; TELEX: 25-3856  
 ; INFORMATION FOR SEQ. ID NO: 45:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 3519 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; FEATURE:  
 ; MOLECULE TYPE: cDNA  
 ; NAME/KEY: CDS  
 ; LOCATION: 52..3519  
 ; US-08-286-889-45  
 Alignment Scores:

Pred. No.: 8.95e-10 Length: 3519  
 Score: 166.00 Matches: 66  
 Percent Similarity: 46.15% Conserved: 42  
 Best Local Similarity: 28.21% Mismatches: 96  
 Query Match: 8.67% Indels: 30  
 DB: 1 Gaps: 12

US-09-970-076-2 (1-368) x US-08-286-889-45 (1-3519)

QY 37 ProAlaCyTyrGly---GlyPheAspLeuTyrPheIleLeuAspLysSerGlySerVal 55  
 DB 481 CCAGAGTGTCCAGGACAAAGAGATGAGACATCTTCTCCGATGATAGCTCCGGCGAGATT 540  
 QY 56 ---LeuHisTyrAsnGluIleTyrTyrPheValGluGlnLeuAlaHisGlyPheIle 74  
 DB 541 GATCAAAAGTACCTTACCCAGATGAAGACTTGTGTCAGAGCTTATGAGCCAGTGGCG 600  
 QY 75 SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys 94  
 DB 601 AGCACACACACCTGCTTCTCCGTATGCAATTAACATCCGAAAGACTCATTTTACC 660  
 QY 95 LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGluGluLeu 109  
 DB 661 TTCACGGAATTCAAGAGCAGCCTGAGCCCTGAGCCTGTGAGTGCATGCTCCAGCTC 720  
 QY 110 GlnLysValLeuProGlyGlyAspThrTyrMetHisGluGlyPheGluArgAlaSerGlu 129  
 DB 721 CAA-----GGCCTGACGTACACAGCCTCGGAGCATCCAGAAAGTGTGAA 765  
 QY 130 GlnIleTyrGluAsnArgGlnGlyTyrArgThrAla---SerValIleIleAlaLeu 148  
 DB 766 GAGCATTTTCATGACAAAGATGCGGCCGGAAGAGTGCAGAAAGATCTATTGTCTATC 825  
 QY 149 ThrAspGlyGluLeuHisGluAspLeuPhePheTyrSerGlu----ArgGluAlaAsn 166  
 DB 826 ACAGATGGCAGAAATTCAGAGACCCCTGAGATGAATGATGATCATCCCTGAACACAG 885  
 QY 167 ArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValLysAsp---PheAsnGlu 185  
 DB 886 AAAGCT-----GGATCATTCCTGATGCTATGAGGAGGAGGAGTCCCTCCGGAA 936  
 QY 186 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhe 199  
 DB 937 CCCACTGCCCTACAGAGACTGAACCATTTGGCTCAGCTCCCTCGACAGACAGCTGTTC 996  
 QY 200 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSer 219  
 DB 997 AAGTGGGCAAT---TTGTGACACTTCGACAGATCCAGCGCAAAATTCAGAGAAA--- 1050  
 QY 220 CysIleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGlySerPheGlnVal 239  
 DB 1051 -----ATCTTGGCATTTGGAAGAACCAATCAAGTCAAGTAGTTCTTTCAGCAC 1101  
 QY 240 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 253  
 DB 1102 GAGATGTCAAGAAAGTTTCAGCTCAGCTCTCTCAATGAT 1143  
 RESULT 4  
 US-08-485-618-45  
 ; Sequence 45, Application US/08485618  
 ; Patent No. 5728533  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gallatin, W. Michael  
 ; APPLICANT: Van der Vieren, Monica  
 ; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit  
 ; NUMBER OF SEQUENCES: 103  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 ; STREET: 233 South Wacker Drive, 6300 Sear Tower  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: United States  
 ; ZIP: 60606-6402

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 52..3519
US-08-485-618-45

Alignment Scores:
Pred. No.: 8,956-10 Length: 3519
Score: 166.00 Matches: 62
Percent Similarity: 46.15% Conservative: 46
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.67% Indels: 30
DB: 1 Gaps: 12

US-09-970-076-2 (1-368) x US-08-485-618-45 (1-3519)
QY 37 ProAlaCyvTYrGly---GlyPheAplLeuTYrPheIleLeuAplYsSerGlySerVal 55
DB 481 CGAGGTGTCCAGGCAAGAGATGAGATGCTTCTCGATGATGAGCTCCGGGAGCAT 540
QY 56 ---LeuHisIleTPraenGluIleTYrTYrPheValGluInLeuAlHisIlePheIle 74
DB 541 GATCAAACTGATTCACCAAGATGAAGACATTCGCAAAAGCTTGATGGGACATTTGCG 600
QY 75 SerProGluInLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys 94
DB 601 AGCACACAGACCTGCTTCTCTGATGCAATCTCAAAACATCTCAAGATCATTTTACC 660
QY 95 LeuThrgluAapArg-----GluGlnIleArgGlnGlyLeuGluGluLeu 109
DB 661 TTCACGGAATTCACAGAGAGCTGAGCCCTGAGACCTCGGAGATGCATGCTCAGCTC 720
QY 110 GlnLysValLeuProGlyGlyAapThryrThryrMetHisGluGlyPheGluArgAlaSerGlu 129
DB 721 CAA-----GGCTGACGTACACAGAGCTCGGAGATCCAGAAAGTGGTGA 765
QY 130 GlnIleTYrTYrGluAapArgGlnIleTYrArgThrAla---SerValIleIleAlaLeu 148
DB 766 GAGGTATTTCTACGACAGATAGGGCCGAGAAATGCGCAAGAGATCTAATTTGTCAT 825
QY 149 ThrAapGlyGluLeuHisGluAapLeuPhePheTYrSerGlu-----ArgGluAlaAsn 166

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DB 826 ACAGATGGCAGAAATTCAGAGACCCCTGAGATATGACATGTCATCCCTGAAGCAGAG 885
QY 167 ArgSerArgAapLeuGlyAlaIleValTYrCyValGlyValLysAap---PheAapGlu 185
DB 886 AAAGCT-----GGATCATCTCGCTATGCTATAGGGGTGGAGATGCTTCGGGAA 936
QY 186 ---ThrgInLeuAlaArgIle-----AlaAapSerLysAapHisValPhe 199
DB 937 CCACACTCCCTACAGAGAGCTGAACACCATTTGGCTGACCTCCCTCGACGACACGCTTTC 996
QY 200 ProValAsnAapGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSer 219
DB 997 AAGGTGGGCAAT---TTGTAGCATCTTCGACGATCCAGCGCGCAAAATTCAGAGAAA--- 1050
QY 220 CysIleGluIleLeuAlaIleGluProSerThrIleCyValAglYsSerPheGlnVal 239
DB 1051 -----ATCTTGGCATTTGAAGAACCAATCAAGTCAGTAAGTACTTCCTTCAGACAC 1101
QY 240 ValValAapGlyAapGlyPheAArgHisAlaArgAapValAap 253
DB 1102 GAGATGTCACAGAAAGCTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 5
US-08-362-652-45
Sequence 45, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vlieten, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 52..3519
US-08-362-652-45

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## Alignment Scores:

Pred. No.:	8,956-10	Length:	3519
Score:	166.00	Matches:	66
Percent Similarity:	46.15%	Conservative:	42
Best Local Similarity:	28.21%	Mismatches:	96
Query Match:	8.67%	Indels:	30
DB:	1	Gaps:	12

US-09-970-076-2 (1-368) x US-08-605-672-45 (1-3519)

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QY 37 ProAlaCyTYrGly---GlyPheAspLeuTYrPheIleLeuAspLySerGlySerVal 55
DB 481 CCAAGTGTCCAGACAGACAGATGACATGCTTCTCGATGATGAGGTCCGGAGCAT 540
QY 56 ---LeuHisHsTPAsnGluIleTYrTYrPheValGluGlnLeuAlaHisLePheIle 74
DB 541 GATCAAAAGTGAATTACCAAGATGAAGACTTCGTCAAAGCTTGATGGCCAGTTGGCG 600
QY 75 SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys 94
DB 601 AGCACACACACCTCTCTCTCTGATGCAATCTCAACATCTGAAAGCTCATTTTACC 660
QY 95 LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGlnGluLeu 109
DB 661 TTCACGGAATTCAGAGACAGACCTGAGCCCTGAGACCTGATGATGATGATGATGATG 720
QY 110 GlnLysValLeuProGlyGlyAspThrTYrMetHisGlnGlyPheGluArgAlaSerGlu 129
DB 721 CAA-----GGCCTGACGTACACAGCCTCGGGCATCAGAAAGTGCGTGA 765
QY 130 GlnIleTYrTYrGlnAsnArgGlnIleTYrArgThrAla---SerValIleIleAlaLeu 148
DB 766 GAGCATTTTCATGCAAGAAATGGGCCCCGAAAGTGCCAGAAAGATCTAATGTCTATC 825
QY 149 ThrAspGlyLeuLeuHisGlnLeuPhePheTYrSerGlu-----ArgGlnAlaAsn 166
DB 826 ACAAGTGGGCAAAATTCAGAGACACCCCTGAGATTAACATGTCATCCCTGAACACAG 885
QY 167 ArgSerArgAspLeuGlyAlaIleValTYrCyValAlGlyValLysAsp---PheAsnGlu 185
DB 886 AAAGCT-----GGGATCATTCGCTATGCTATAGGGGTGGAGATGCCCTCCGGGAA 936
QY 186 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhe 199
DB 937 CCCACTGCTTACAGAGACCTGAACACCATGGCTGACCTCCCTGACAGACCATGTTTC 996
QY 200 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysLysSer 219
DB 997 AAGGTGGGCAT---TTGTAGCACTTCGACGATCCAGCGCAATTCAGAGAAA--- 1050
QY 220 CyValGluIleLeuAlaAlaGluProSerThrIleCyValAlGlyGluSerPheGlnVal 239
DB 1051 -----ATCTTGGCATTGTAAGAACCGAATCAAGTCAAGTATCTTTTCAGACAC 1101
QY 240 ValValArgGlyAsnGlyPheArgHisAlaAlaAsnValAsp 253
DB 1102 GAGATGTCAACAAGAGTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 6
US-08-605-672-45
; Sequence 45, Application US/08605672
; Patent No. 5817515
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois

```

```

; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,672
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3519 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 52..3519
; US-08-605-672-45

Alignment Scores:
Pred. No.: 8,956-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.67% Indels: 30
DB: 1 Gaps: 12

US-09-970-076-2 (1-368) x US-08-605-672-45 (1-3519)
QY 37 ProAlaCyTYrGly---GlyPheAspLeuTYrPheIleLeuAspLySerGlySerVal 55
DB 481 CCAAGTGTCCAGACAGACAGATGACATGCTTCTCGATGATGAGGTCCGGAGCAT 540
QY 56 ---LeuHisHsTPAsnGluIleTYrTYrPheValGluGlnLeuAlaHisLePheIle 74
DB 541 GATCAAAAGTGAATTACCAAGATGAAGACTTCGTCAAAGCTTGATGGCCAGTTGGCG 600
QY 75 SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys 94
DB 601 AGCACACACACCTCTCTCTGATGCAATCTCAACATCTGAAAGCTCATTTTACC 660
QY 95 LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGlnGluLeu 109
DB 661 TTCACGGAATTCAGAGACAGACCTGAGCCCTGAGACCTGATGATGATGATGATGATG 720
QY 110 GlnLysValLeuProGlyGlyAspThrTYrMetHisGlnGlyPheGluArgAlaSerGlu 129
DB 721 CAA-----GGCCTGACGTACACAGCCTCGGGCATCAGAAAGTGCGTGA 765
QY 130 GlnIleTYrTYrGlnAsnArgGlnIleTYrArgThrAla---SerValIleIleAlaLeu 148
DB 766 GAGCATTTTCATGCAAGAAATGGGCCCCGAAAGTGCCAGAAAGATCTAATGTCTATC 825

```

```

OY      149   ThisArgLUGUjLeHnIeGlvAryLeuherNeTUsertGlu-----ArgGlunAlaasn 166
           |||||.....|||||
Db       826   ACGATGGAGCCAAATTCAAGACACCCCCCGAGGTATACATGTATGCCCTGAAGACAG 885
           |||||.....|||||
OY      167   ArgSerAaGvArLeuGLyAlaAlaValTyTCySvAlGIvAllyuAsP---PhenAnglu 185
           ::::.....:|||||
Db       886   AAAGCT-----GGGATCATTCGCTATGTGTAAGGGGTGGAGATGCCTCCGGGAA 936
           |||||.....|||||
OY      186   ---ThrGlnLeuAlaArgLe-----AlaSerSetLyAsPArHisValPhe 199
           |||||.....|||||
Db       937   CCCATGCGCCSTACAGAGACTGAACACATTTGGCTCAGCTCCCTCCGACAGACCAACGCTTTC 996
           |||||.....|||||
OY      200   ProValaaNArGLyPhcGlnAlaLeuGngInGylleIHeserIlleuNyVyrSer 219
           |||||.....|||||
Db       997   AAGGTGGGCAT---TTTGTCACACTTCCGACATCCAGCGCAATTCAAGAGAAA--- 1055
           |||||.....|||||
OY      220   CyvIlegluIleLeuAlaAlaGluProSerThrIleCyvAlaglyGluSerPheGlnVal 239
           |||||.....|||||
Db       1051  -----ATCTTTGCCATTGAAGAACCGAATCAAGTCAAGTAGTCTTTTCAGCAC 1101
           |||||.....|||||
OY      240   ValValaTgGlyAnGlyPhcArgHisValaGvaenValaP 253
           ::::|||...|||
Db       1102  GAGATGTCAACAAGAGTTTTCAGCTCAGCTCTTCATGAT 1143
           |||||.....|||||

RESULT 7
US-08-482-293A--45
; Sequence 45, Application US/08482293A
; Patent No. 5831029
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5831029e1 Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borum
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,293A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27666/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3519 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 52..3519
US-08-482-293A-45

Alignment Scores:
Pred. No.:      8,95e+10      Length:      3519
Score:          166.00        Matches:      66
Percent Similarity: 46.15%    Conservative: 42
Best Local Similarity: 28.21% Mismatch:      96
Query Match:      8.67%       Indels:       30
DBs:              2           Gaps:         12

US-09-970-076-2 (1-368) x US-08-482-293A-45 (1-3519)
QY      37 ProLaAcYrTgryGly---GlyPheAspLeuTyRpheIleLeuApLySergLySerVal 55
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      481 CCAGAGTGTCACAGACAAGAATGACATTCCTCCCGATGTGATGGCTCCGGCAGCATTT 540
QY      56 ---LeuHisTrpAsnGluLileTyTyRpheValGluInLeuAlaHisLyPheIle 74
      :::: :::::: :::::: :::::: :::::: :::::: :::::: ::::::
Db      541 GATCAAAAGTAGCTTTACCACAGATAMAGACTTCTCTCAAAGCTTTGATGGCCAGTTGGCG 600
QY      75 SerProGlnLeuArGmetSerPheIleValPheSerThrArgGlyThrThrLeuMetLyS 94
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      601 AGCACCCAGCACCTCGTTCTCCCTGATGCATACTCAAACATCTCGAAGACTCATTTTACC 660
QY      95 LeuThrGluAparG-----GluGlnIleArgGlnGlyLeuGluGluLeu 109
      ||||| ||||| :::: :::: :::: :::: :::: :::: ::::
Db      661 TTCACGAATTCCAGAGACGCCCTACGCCCTCAGAGCCTGTCGATGGCATGCTGCACCTC 720
QY      110 GlnLyValLeuProGlyGlyAspThrTyRmethIsGluGlyPheGluArgAlaSerGlu 129
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      721 CA-----GGCTGACGTACACAGACTCGGGCATCCAGAAAAGTGTGAAA 765
QY      130 GlnIleTyTyRGluAenArgGlnGlyTyRArgThrAla---SerValIleIleAlaLeu 148
      :::::: :::::: :::::: :::::: :::::: :::::: :::::: ::::::
Db      766 GAGCTATTTCATTCACAGATAGGGGCCCGAAAAAGTCCAGAAAGATTAATTGTCTATC 825
QY      149 ThrAspGlyGluLeuHisGluAspLeuPhePheTyRserGlu-----ArgGluAlaasn 166
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      826 ACAGATGGGCGAATTCACAGACCCCCCTGAGATATAGACATGTCATCCCTCGAAGCAGAG 885
QY      167 ArgSerArgAspLeuGlyAlaIleValTyTCysValGlyValLyAsp--PheAsnGlu 185
      :::::: :::::: :::::: :::::: :::::: :::::: :::::: ::::::
Db      886 AAAGCT-----GGGATCATTCGGCTATGAGGGGGTGGAGATGCTTCGGGGAA 936
QY      186 ---ThrGlnLeuAlaArgIle-----AlaAspSerLyAspHisValPhe 199
      :::::: :::::: :::::: :::::: :::::: :::::: :::::: ::::::
Db      937 CCCACATGGCCCTACAGAGACTGACACCAATGGCTGCACCTCCCTCGAGAACACAGCTGTCTC 996
QY      200 ProValAsnaAspGlyPheGlnAlaLeuGlnGlyLileIleHiserIleLeuLyLySer 219
      :::::: :::::: :::::: :::::: :::::: :::::: :::::: ::::::
Db      997 AAGGTGGGCAT--TTTGTGACCTTCGCGACATCCAGCGCGCAATTCAGAGAA-- 1050
QY      220 CysIleGluIleLeuAlaValagLuproSerThrIleCySalagLyusErPheGlnVal 239
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1051 -----ACTTTGCCATTGAAAGAAACCAATCAAGGTCAAGATGTCCTTCACAGAC 1101
QY      240 ValValArgLyAsnGlyPheArgHisAlaArgAsnValAsp 253
      :::::: :::::: :::::: :::::: :::::: :::::: :::::: ::::::
Db      1102 GAGATGTCAAGAAAGTTTCAGCTCAGCTCTCTCAATGTAT 1143

RESULT 8
US-08-943-363-45
; Sequence 45, Application US/08943363
; Patent No. 5837478
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; TITLE OF INVENTION: Van der Vieren, Monica
; NUMBER OF SEQUENCES: 114

```



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Dh 721 CAA-----GGCCTGACGTACACAGCCTCGGGCATCCGAAAGTGTGAAA 765
Oy 130 GlnleYrYrYrgUaMaArGInGInGlyYrArGhrAla---SerValIleIleAlaIeu 148
Dh 766 GAGCTATTTCATTCAGCAAGAAATGGGGCCCGAAAGAGTCCAGAAAGATTAATTGTCATC 825
Oy 149 ThrApGrlYglUeuHtIsGluApLeuPhePheTyrSerGlu-----ArgGluAlaAsn 166
Dh 826 ACAAGATGGGCGAAATTCACAGACCCCTGTGAGTATAGACATGTCATCCCTGAAAGCAGAG 885
Oy 167 ArgSerArGApLeuGlyAlaAlaIleValYrCySvalGlyValIyAsp---PheAsnGlu 185
Dh 886 AAAGCT-----GGATCATTCGCGTATGCTATAGGGGGGGAGATGCTTCGGGAAA 936
Oy 186 ---ThrGlnleuAlaAaGlie-----AlaAspSerIyAspHisValPhe 199
Dh 937 CCCATCCCTCCCTACAGAGCTGAAACACCATTTGGCTCACTCCCTGCGAGGACAGTGTTC 996
Oy 200 ProValaMaApGrlYpHeGlnAlaIeuGInGlyIleIleHisSerIleUeuIyLeuSer 219
Dh 997 AAGGTGGGCAT---TTTGTACACTTCGCGAGCATCCAGCGCAAAATTCAGAGAAA--- 1050
Oy 220 CySleIleGluIleUeuAlaAaGluProSerThrIleCySlaGlyIuSerPheGlnVal 239
Dh 1051 -----ATCTTTGGCATTTGAAGAAAGAACGAAATCAAGTCAAGTACTTCTTCAGGAC 1101
Oy 240 ValValaArgGlyAaengIyPheArGHisAlaAArgAsnValAsp 253
Dh 1102 GAGATGTCAACAGAGGTTTCAGCTCAGCTCATGTGAT 1143

RESULT 9
US-09-193-043-45
; Sequence 45, Application US/09193043
; Patent No. 6251395
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 6251395el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/193, 043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173, 497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286, 889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362, 652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943, 363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52) .. (3516)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-193-043-45

Alignment Scores:
Pred. NO.: 8,95e-10 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.67% Indels: 30
DB: 3 Gaps: 12

US-09-970-076-2 (1-368) x US-09-193-043-45 (1-3519)
37 ProAlaCySfYrGly---GlyPheAspLeuYrPheIleUeuApIySergIySerVal 55

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Db 481 CCAGAGTGTCCAGAGCAAGAGATGACATTTGCTTCCGATGATGAGGCTCCGGACGACTT 540
Oy 56 ---LeuHsiHstPrAengGluIleTyTrPheValGluGlnLeuAlaHieLysPheIle 74
Db 541 GATCAAGTGAATTCATCCAGATGAAGACTTCGTAAGCTTTGATGATGGCCAGTGGCG 600
Oy 75 SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys 94
Db 601 AGCACACAGACACCTGCTCTCCCTGATGCAATGACTCAAAACATCCGTAAGACTCATTTTACC 660
Oy 95 LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGluGlnLeu 109
Db 661 TTCACGGAATTCACAGACAGCCCTGAGCCCTGAGACCCCTGGATGGATGCTCCAGCTC 720
Oy 110 GlnLysValLeuProGlyLysPheThrTyrmethIleGluGlyPheGluArgAlaSerGlu 129
Db 721 CAA-----GGCTGACGTACACAGCTCGGGCATCCAGAAAGTGCTGA 765
Oy 130 GlnIleTyTrGluAsnArgGlnGlyTyTrArgThrAla---SerValIleIleAlaLeu 148
Db 766 GAGCTATTTCATACAGAGATGGGGCCGAAAGAGTCCGAAAGATATCTATTGTCTATC 825
Oy 149 ThrArgGlyGluLeuHieGlnLysPhePheTyTrSerGlu-----ArgGluAlaAsn 166
Db 826 ACAGATGGGCAGAAATTCAGAGACCCCTGAGATGACATGTCATCCTGAAAGCAGAG 885
Oy 167 ArgSerArgAspLeuGlyAlaIleValTyTrCysValGlyValLysAsp---PheAsnGlu 185
Db 886 AAAGCT-----GGATCATTTGGCTATGCTATAGGGGTGGAGATGCTTCGGGAA 936
Oy 186 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHieValPhe 199
Db 937 CCCACTGCCCTACAGAGACTGAACACCATTTGGCTCAGCTCCCTCGCAGACACAGCTGTTCC 996
Oy 200 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHieSerIleLeuLysSer 219
Db 997 AAGGTGGGCAAT---TTTGTAGCACTTCGACGACATCCGCGCAATTCAGAGAA--- 1050
Oy 220 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyLysPheGlnVal 239
Db 1051 -----ATCTTTGCCATTGAAAGAACCAATGACATGACATGATCTCTTCACGAC 1101
Oy 240 ValValArgGlyAsnGlyPheArgHieValArgAsnValAsp 253
Db 1102 GAGATGTCACAAAGAGTTTCAGCTCAGCTCTCATGAT 1143

RESULT 10
US-09-688-307A-45
; Sequence 45, Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; TITLE OF INVENTION: No. 6432404el Human Beta-2
; FILE REFERENCE: 27866/36646
; CURRENT APPLICATION NUMBER: US/09/688.307A
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193.043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605.672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173.497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286.889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362.652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943.363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 45
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; LENGTH: 3519
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(3516)
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-688-307A-45

Alignment Scores:
Pred. No.: 8.95e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.67% Indels: 30
DB: 4 Gaps: 12

US-09-970-076-2 (1-368) x US-09-688-307A-45 (1-3519)
Oy 37 ProAlaCysTyTrGly---GlyPheAspLeuTyTrPheIleLeuAspLysSerGlySerVal 55
Db 481 CCAGAGTGTCCAGAGCAAGAGATGACATTTGCTTCCGATGATGAGGCTCCGGACGACTT 540
Oy 56 ---LeuHsiHstPrAengGluIleTyTrPheValGluGlnLeuAlaHieLysPheIle 74
Db 541 GATCAAGTGAATTCATCCAGATGAAGACTTCGTAAGCTTTGATGATGGCCAGTGGCG 600
Oy 75 SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys 94
Db 601 AGCACACAGACACCTGCTCTCCCTGATGCAATGACTCAAAACATCCGTAAGACTCATTTTACC 660
Oy 95 LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGluGlnLeu 109
Db 661 TTCACGGAATTCACAGACAGCCCTGAGCCCTGAGACCCCTGGATGGATGCTCCAGCTC 720
Oy 110 GlnLysValLeuProGlyLysPheThrTyrmethIleGluGlyPheGluArgAlaSerGlu 129
Db 721 CAA-----GGCTGACGTACACAGCTCGGGCATCCAGAAAGTGCTGA 765
Oy 130 GlnIleTyTrGluAsnArgGlnGlyTyTrArgThrAla---SerValIleIleAlaLeu 148
Db 766 GAGCTATTTCATACAGAGATGGGGCCGAAAGAGTCCGAAAGATATCTATTGTCTATC 825
Oy 149 ThrArgGlyGluLeuHieGlnLysPhePheTyTrSerGlu-----ArgGluAlaAsn 166
Db 826 ACAGATGGGCAGAAATTCAGAGACCCCTGAGATGACATGTCATCCTGAAAGCAGAG 885
Oy 167 ArgSerArgAspLeuGlyAlaIleValTyTrCysValGlyValLysAsp---PheAsnGlu 185
Db 886 AAAGCT-----GGATCATTTGGCTATGCTATAGGGGTGGAGATGCTTCGGGAA 936
Oy 186 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHieValPhe 199
Db 937 CCCACTGCCCTACAGAGACTGAACACCATTTGGCTCAGCTCCCTCGCAGACACAGCTGTTCC 996
Oy 200 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHieSerIleLeuLysSer 219
Db 997 AAGGTGGGCAAT---TTTGTAGCACTTCGACGACATCCGCGCAATTCAGAGAA--- 1050
Oy 220 CysIleGluIleLeuAlaIleGluProSerThrIleCysAlaGlyLysPheGlnVal 239
Db 1051 -----ATCTTTGCCATTGAAAGAACCAATGACATGACATGATCTCTTCACGAC 1101
Oy 240 ValValArgGlyAsnGlyPheArgHieValArgAsnValAsp 253
Db 1102 GAGATGTCACAAAGAGTTTCAGCTCAGCTCTCATGAT 1143

RESULT 11
US-09-350-259-45
; Sequence 45, Application US/09350259
; Patent No. 6620915
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
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Alignment Scores:	
Pred. No.:	8.95e-10
Score:	166.00
Percent Similarity:	46.15%
Best Local Similarity:	28.21%
Query Match:	8.67%
DB:	4
Gaps:	12

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Oy      200  ProValenAepgIyPheGInAlaLengInclYleIleHISserIleLeuYsIySer 219
          |||:::|||||:::|||||:::|||||:::|||||
Db      997  AAGGTGGGCAAT---TTGTGACACTTCGCGACATCCAGCGGCAATTACAGAGAAA--- 1055
          |||:::|||||:::|||||:::|||||

Oy      220  CysIleGtuIleuAlaIaGluProSerThrIleCysAlaGlyGluSerPheGInVal 239
          |||:::|||||:::|||||:::|||||
Db      1051 -----ACCTTTGGCATTGAGGAACCGAATCAAGTCAAGTAGTCTTCACGAC 1101
          |||:::|||||:::|||||:::|||||

Oy      240  ValValAlArgIyAenGlyPheArgHISAlArGseNValAaP 253
          :::|||||:::|||||:::|||||
Db      1102  GAGATGTCACAAAGGTTTCAGCTCAGCTCTCAATGAT 1143
          :::|||||:::|||||:::|||||

RESULT 12
; Sequence 52, Application US/08485618
; Patent No. 5728533
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 57285333el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Seear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,618
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32797
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3803 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3486
; US-08-485-618-52

Alignment Scores:
Pred. NO.: 1.02e-09 Length: 3803
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8.67% Indels: 30

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US-09-970-076-2 (1-368) x US-08-485-618-52 (1-3803)
US-08-362-652-52
US-08-362-652-52
Sequence 52, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEO ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 3803 base pairs
type: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3486
US-08-362-652-52

Alignment Scores:
Pred. No.: 1,02e-09 Length: 3803
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 8,67% Indels: 30
DB: 1 Gaps: 12

US-09-970-076-2 (1-368) x US-08-362-652-52 (1-3803)
QY      37      ProAlAGyeTyGly---GlyPheAspLeuTyrPheIleuAAspLySerGlySerVal 55
       |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
Db      430      CCAGAATGTCCAGACAGACAAGATGACACTTGCTTCTCGATGATTGGCTCCGCCAGCAT 488
QY      56      ---LeuHnHtAPrsnglnlLeTyTrPheValglnIleuAlHnLylvPheIle 74
               :::::  |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
Db      490      GATCAAAAGTAGCTTAACCAAGATGAAGAGACTTCGTAAGCTTTGATGGGCGC 549
QY      75      SerPrGlnLeuAyrMecSerPheIleValPheSerThrArgIlyThrIleuMeLyS 94
               :::::  |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
Db      550      AGCACACAGACACTCGTTCTCCCTGATGCATACTCAACATCTCGAAGACTCATTTACC 609
QY      95      LeuThrcGluaAspArg-----GluGlnIleArgGlnIlyLeuGlnIlyLeu 109
           |||||   |||   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  |||   |||   |||
Db      610      TTCACGGAAATTCAGAAGCAGCCTTGAGCCCTCAGAGCCTGGTGATGCCATGCTCAGACT 668
QY      110     GlnLysValIleuProGlyGlyAAspThrTyTMechIsglnIyPhegluArgAlaSerGlu 129
           |||||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
Db      670      CAA-----GGCTGACGTRKACACAGCTCGGCCATCCAGAAAGTGTAAA 714
QY      130     GlnLetyTyrgLnAsnArgGlnIlyTyrrArgThrAla--SerValIleIleAlau 148
           :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db      715      GAQCTATTTCATVACAGAACAAATGGGGCGCCGAAAAAGTCCAGAGAAATCATTAATGTCATC 774
QY      149     ThrAspGlyGlnIleuHnIsglnAspLeurebhePheTyrsargIu-----ArgGluAlaAsn 166
           |||||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
Db      775      ACAGATGGGCAAAAATTCAGAACACCCCTCGAGATGATGACATGTCATCCCTGAAGCAGAG 834
QY      167     ArgSerArxAspLeuGlyAlaIleValTyrcyAvAlGlyVallyAsp---PheAsnGlu 185
           :::::  :::::  |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||
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QY      186     ---ThGlnIleuAlaArgIle-----AlaAspSerLyAspHnIsvAlPhe 199

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D	b		886	CCCACTGCCCTTCAGSAGACTGAAACCACTTGGCTCAGCTCCCTCCAGAGCACCATGTTC	945
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Oy			220	CysIleGluIleLeuAlaIlaGluProSerThrIleCyValaGlyGluSerPheGlnVal	239
D	b		1000	-----ATCTTTCGCACTTGGAAGAACCAGATCAAGTCAAGTAGTCTTTTCAGCAC	1050
Oy			240	ValValaArgGlyAenGlyPheArgHISAlaArgAsnValASP	253
D	b		1051	GAGATGTCAACAAGAGTTTCAGCTCAGCTCTCTCAATGAT	1092
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			Patent No. 5817515		
			GENERAL INFORMATION:		
			APPLICANT: Gallatin, W. Michael		
			APPLICANT: Van der Vieren, Monica		
			TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit		
			NUMBER OF SEQUENCES: 103		
			CORRESPONDENCE ADDRESS:		
			ADDRESSSEE: Marshall, O'Toole, Gerstein, Murray & Borun		
			STREET: 233 South Wacker Drive, 6300 Sear Tower		
			CITY: Chicago		
			STATE: Illinois		
			COUNTRY: United States		
			ZIP: 60606-6402		
			COMPUTER READABLE FORM:		
			MEDIUM TYPE: Floppy disk		
			COMPUTER: IBM PC compatible		
			OPERATING SYSTEM: PC-DOS/MS-DOS		
			SOFTWARE: Patent Release #1.0, Version #1.25		
			CURRENT APPLICATION DATA:		
			APPLICATION NUMBER: US/08/605,672		
			FILING DATE:		
			CLASSIFICATION: 530		
			PRIOR APPLICATION DATA:		
			APPLICATION NUMBER: US 08/173,497		
			FILING DATE: 23-DEC-1993		
			PRIOR APPLICATION DATA:		
			APPLICATION NUMBER: US 08/286,889		
			FILING DATE: 5-AUG-1994		
			PRIOR APPLICATION DATA:		
			APPLICATION NUMBER: US 08/362,652		
			FILING DATE: 21-DEC-1994		
			ATTORNEY/AGENT INFORMATION:		
			NAME: Williams Jr., Joseph A.		
			REGISTRATION NUMBER: 38,659		
			REFERENCE/DOCKET NUMBER: 27866/32684		
			TELECOMMUNICATION INFORMATION:		
			TELEPHONE: 312-474-6300		
			TELEFAX: 312-474-0448		
			TELEX: 25-3856		
			INFORMATION FOR SEQ ID NO: 52:		
			SEQUENCE CHARACTERISTICS:		
			LENGTH: 3803 base pairs		
			TYPE: nucleic acid		
			STRANDEDNESS: single		
			TOPOLOGY: linear		
			MOLECULE TYPE: cDNA		
			FEATURE:		
			NAME/KEY: CDS		
			LOCATION: 1..3486		
			US-08-605-672-52		
 Alignment Scores:					
			Pred. No.: 1,02e-09		Length: 3803
			Score: 166.00		Matches: 66
			Percent Similarity: 46.15%		Conservative: 42

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Best Local Similarity: 28.21%
Query Match: 8.67%
DB: 1
US-09-970-076-2 (1-368) x US-08-605-672-52 (1-3803)

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QY 56 ---LeuHsiSTRPaenGluIleTYrTYrPheValGluInleuAhiLeuPheIle 74
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QY 149 ThrArgGlyGluLeuHisGluAspLeuPheIleTYrSerGlu-----ArgGluAlaAsn 166
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QY 167 ArgSerArGAspLeuGlyAlaIleValTYrCysValGlyValIysAsp---PheAsnGlu 185
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QY 220 CysIleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyLysSerPheGluVal 239
DB 1000 -----ATCTTTGGCCATTGAAAGAAACCAATCAAGATCAAGTCACTTCCTTCAGCAC 1050
QY 240 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 253
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RESULT 15
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; Sequence 52, Application US/08482293A
; Patent No. 5831029
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vliet, Monica
; TITLE OF INVENTION: No. 5831029e1 Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6500 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,293A  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3803 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..3486  
US-08-482-293A-52  
  
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Score: 166.00 Matches: 66  
Percent Similarity: 46.15% Conservative: 42  
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QY 75 SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys 94  
DB 550 AGCACCAGACACTCTCTCTCTGATGCAATCTCAACATCTGAAGATCATTTTACC 609  
QY 95 LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGluGluLeu 109  
DB 610 TTCACGGAATTCAGAGCAGCTGAGCCCTGAGAGCTGTGTGATGCATCTCCAGCTC 669  
QY 110 GlnLysValIleuProGlyGlyAspThrTyrMetH18GluGlyPheGluArgAlaSerGlu 129  
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QY 130 GlnIleTyrTyrGluAsnArgGlnGlyTyrArgThrAla---SerValIleIleAlaLeu 148  
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QY 149 ThrAspGlyGluLeuH18GluAspLeuPhePheTyrSerGlu-----ArgGluAlaAsn 166  
DB 775 ACAGATGGCGCAGAAATTCAGAGACCCCTGTGATATAGACATGTCACTCCCTGAACAGAG 834

QY 167 ArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValLysAsp---PheAsnGlu 185  
DB 835 AAAGCT-----GGGATCATTTCCGCTATATAGGGGTGGAGATGCTTCGGGGA 885  
QY 186 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspH18ValPhe 199  
DB 886 CCACATCCCTTACAGAGCTGAACACCATTTGGCTCAGCTCCCTGCGAGACAGTGTTC 945  
QY 200 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleH18SerIleLeuLysSer 219  
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Job time : 95.151 secs

GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 22, 2004, 01:18:40 ; Search time 72.528 Seconds

(without alignments)  
2547.963 Million cell updates/sec

Title: US-09-970-076-8

Perfect score: 1728  
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Searched: 682709 segs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
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Listing first 45 summaries

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6: /cg2\_6/ProdData/2/lna/Backfillse1.seg:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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1	1728	100.0	2459	4	US-09-833-381-998 Sequence 998, App
2	1392	80.6	1609	4	US-09-620-312D-8 Sequence 8, Appl
3	166	9.6	3519	1	US-08-286-889-45 Sequence 45, Appl
4	166	9.6	3519	1	US-08-485-618-45 Sequence 45, Appl
5	166	9.6	3519	1	US-08-362-652-45 Sequence 45, Appl
6	166	9.6	3519	1	US-08-605-672-45 Sequence 45, Appl
7	166	9.6	3519	1	US-08-482-293A-45 Sequence 45, Appl
8	166	9.6	3519	2	US-08-943-363-45 Sequence 45, Appl
9	166	9.6	3519	3	US-09-193-043-45 Sequence 45, Appl
10	166	9.6	3519	4	US-09-688-307A-45 Sequence 45, Appl
11	166	9.6	3519	4	US-09-350-259-45 Sequence 45, Appl
12	166	9.6	3803	1	US-08-485-618-52 Sequence 52, Appl

13	166	9.6	3803	1	US-08-362-652-52 Sequence 52, Appl
14	166	9.6	3803	1	US-08-605-672-52 Sequence 52, Appl
15	166	9.6	3803	2	US-08-482-293A-52 Sequence 52, Appl
16	166	9.6	3803	2	US-08-943-363-52 Sequence 52, Appl
17	166	9.6	3803	3	US-09-193-043-52 Sequence 52, Appl
18	166	9.6	3803	4	US-09-688-307A-52 Sequence 52, Appl
19	166	9.6	3803	4	US-09-350-259-52 Sequence 52, Appl
20	159.5	9.2	2499	1	US-08-485-618-96 Sequence 96, Appl
21	159.5	9.2	2499	1	US-08-605-672-96 Sequence 96, Appl
22	159.5	9.2	2499	2	US-08-482-293A-96 Sequence 96, Appl
23	159.5	9.2	2499	2	US-08-943-363-96 Sequence 96, Appl
24	159.5	9.2	2499	3	US-09-193-043-96 Sequence 96, Appl
25	159.5	9.2	2499	3	US-09-688-307A-96 Sequence 96, Appl
26	159.5	9.2	2499	4	US-09-350-259-96 Sequence 96, Appl
27	159.5	9.2	3528	1	US-08-286-889-36 Sequence 36, Appl
28	159.5	9.2	3528	1	US-08-485-618-36 Sequence 36, Appl
29	159.5	9.2	3528	1	US-08-362-652-36 Sequence 36, Appl
30	159.5	9.2	3528	1	US-08-605-672-36 Sequence 36, Appl
31	159.5	9.2	3528	2	US-08-482-293A-36 Sequence 36, Appl
32	159.5	9.2	3528	2	US-08-943-363-36 Sequence 36, Appl
33	159.5	9.2	3528	3	US-09-193-043-36 Sequence 36, Appl
34	159.5	9.2	3528	4	US-09-688-307A-36 Sequence 36, Appl
35	159.5	9.2	3528	4	US-09-350-259-36 Sequence 36, Appl
36	159.5	9.2	3597	1	US-08-485-618-54 Sequence 54, Appl
37	159.5	9.2	3597	1	US-08-362-652-54 Sequence 54, Appl
38	159.5	9.2	3597	1	US-08-605-672-54 Sequence 54, Appl
39	159.5	9.2	3597	2	US-08-482-293A-54 Sequence 54, Appl
40	159.5	9.2	3597	2	US-08-943-363-54 Sequence 54, Appl
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45	159.5	9.2	3726	1	US-08-286-889-1 Sequence 1, Appl

## ALIGNMENTS

## RESULT 1

US-09-833-381-998  
; Sequence 998, Application US/09833381  
; Patent No. 6672186  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: NO. 6672186el Nucleic Acid and Protein Homologs  
; FILE REFERENCE: 5800-119  
; CURRENT APPLICATION NUMBER: US/09/833,381  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: 09/516,448  
; PRIOR FILING DATE: 2000-02-29  
; NUMBER OF SEQ ID NOS: 2050  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 998  
; LENGTH: 2459  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc\_feature  
; LOCATION: (1) ... (2459)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-833-381-998

## Alignment Scores:

Pred. No.: 2.79e-213 Length: 2459  
Score: 1728.00 Matches: 333  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-970-076-8 (1-333) x US-09-833-381-998 (1-2459)

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Db      472 CTGGTGCTCATTCGGCCGGGCGAGGGGAGCGCAGAGAGATGGGGTCCAGCTGCTAC 531
Qy      41  GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTyrAsn 60
Db      532 GCGCGATTGACCTGTACTTCATTTTGGACAATCAGAGAGGTGCTGCACACCTGGAAT 591
Qy      61  GluIleTyrTyrPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMet 80
Db      592 GAAATCTATTACTTGTGGAGACGTTGGCTCAAAATTCATCAGCCACAGTTGGAATG 651
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Qy      121  HisGluGlyPheGluIuArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140
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Qy      141  ThrAlaSerValIleIleAlaLeuThrAspGlyGluLeuHisGluAspLeuPhePheTyr 160
Db      832 ACAGCCAGGCTCATCTTGTGCTTGTGACTGATGAGAACTCCATGAAAGATCTCTTTTCTAT 891
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/ APPLICANT: Aesudi, Vinod
/ APPLICANT: Zhang, Jie
/ APPLICANT: Ren, Feiyan
/ APPLICANT: Chen, Rui-hong
/ APPLICANT: Zhao, Qing A.
/ APPLICANT: Weinman, Tom
/ APPLICANT: Xue, AIdong J.
/ APPLICANT: Yang, Yonghong
/ APPLICANT: Wang, Jian-Rui
/ APPLICANT: Zhou, Ping
/ APPLICANT: Ma, Yungqing
/ APPLICANT: Wang, Dunrui
/ APPLICANT: Wang, Zhiwei
/ APPLICANT: John Tillinghast
/ APPLICANT: Drmanac, Radoje T.
/ TITLE OF INVENTION: No. 659662el Nucleic Acids and
/ TITLE OF INVENTION: Polypeptides
/ FILE REFERENCE: 784CIP28
/ CURRENT APPLICATION NUMBER: US/09/620,312D
/ CURRENT FILING DATE: 2000-07-19
/ PRIOR APPLICATION NUMBER: 09/552,317
/ PRIOR FILING DATE: 2000-04-25
/ PRIOR APPLICATION NUMBER: 09/488,725
/ PRIOR FILING DATE: 2000-01-21
/ NUMBER OF SEQ ID NOS: 1105
/ SOFTWARE: pc_fl_genes Version 1.0
/ SEQ ID NO 8
/ LENGTH: 1609
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (309)..(1202)
/ US-09-620-312D-8
/
Alignment Scores:
Pred. No.: 4,81e-170 Length: 1609
Score: 1392.00 Matches: 267
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 99.26% Mismatches: 0
Query Match: 80.56% Indels: 0
Gaps: 0
/
US-09-970-076-8 (1-333) x US-09-620-312D-8 (1-1609)
Qy      1  MetAlaThrAlaGluAspArgAlaLeuGlyTyrGlyPheGlnTyrLeuSerLeuAlaThr 20
Db      309  ATGCCACGGCGGAGCGGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT 368
Qy      21  LeuValLeuIleCyAlaGlyGlnGlyArgArgIuAspGlyGlyProAlaCysTyr 40
Db      369  CTGGTGCTCATTCGGCCGGGCGAGGGGAGCGCAGAGAGATGGGGTCCAGCTGCTAC 428
Qy      41  GlyGlyPheAspLeuTyrPheIleLeuAspLysSerGlySerValLeuHisIleTyrAsn 60
Db      429  GCGCGATTGACCTGTACTTCATTTTGGACAATCAGAGAGGTGCTGCACACCTGGAAT 488
Qy      61  GluIleTyrTyrPheValGluGlnLeuAlaHisIlePheIleSerProGlnLeuArgMet 80
Db      489  GAAATCTATTACTTGTGGAGACGTTGGCTCAAAATTCATCAGCCACAGTTGGAATG 548
Qy      81  SerPheIleValPheSerThrArgGlyThrThrLeuMetLysLeuThrGluAspArgGlu 100
Db      549  TCCTTATTGTTTCTCCACCCGAGAGAACCTTAATGAACCTGACAGAAAGACAGAGA 608
Qy      101  GlnIleArgGlnGlyLeuGlnGluLeuGlnLysValLeuProGlyGlyAspThrTyrMet 120
Db      609  CAATCCGTCAGAGGCTAGAGAGACTCCAGAAAGTTTCCGAGAGAGACACTTACATG 668
Qy      121  HisGluGlyPheGluIuArgAlaSerGluGlnIleTyrTyrGluAsnArgGlnGlyTyrArg 140
Db      669  CATGAAGATTTGAAAGGCGCCAGTAGCAGATTATTATGAAACAGCAAGGGGTACAGG 728

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RESULT 2
US-09-620-312D-8
/ Sequence 8, Application US/09620312D
/ Patent No. 6569662
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Liu, Chenghua

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QY 141 ThrAlaSerValIleIleAlaLeuThraPheArgIleuLeuHleuAlaPheLeuPhePheTyr 160
DB 729 ACAGCAGAGGTCATCTTCTTGAATGAGAACTCCAGAGATCTCTTTCTAT 788
QY 161 SerGluArgGluAlaAsnArgSerArgPheLeuGluAlaIleValTyrCyValGluVal 180
DB 789 TCAGAGAGAGGAGCTTAATGATCTCGAGATCTTGAGCAATGTTACTGTTGCTGGTG 848
QY 181 LysAspPheAsnGluThrGlnLeuAlaArgIleAlaAspSerLysAspHisValPhePro 200
DB 849 AAAGATTTCATGAACACAGAGCTGGCCGATGGGAGAGAGATCATGTGTTTCCC 908
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSerCys 220
DB 909 GCGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCTCAATTTTGAAGAAGTCTTCC 968
QY 221 IleguIleLeuAlaAlaGluProSerThrIleCysAlaGlyLysSerPheGlnValVal 240
DB 969 ATCGAAATTCAGACAGTCACATCCATCATGAGAGAGATTCATTCAGTTGTC 1028
QY 241 ValAlaGlyAlaGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheLys 260
DB 1029 GCGAAGAGAAAGCGCTTCGACATGCGCGCAAGTGGACAGGCTCTGCAAGTTTCAAG 1088
QY 261 IleAsnAspSerValThrLeuAsnGlu 269
DB 1089 ATCAATGACTCGCTCACACTCAGTAAAG 1115

RESULT 3
US-08-286-889-45
; Sequence 45, Application US/08286889
; Patent No. 5470953
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Mich
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
; STREET: 233 South Wacker Drive, 6300 Seear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,889
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: P38,659
; REFERENCE/DOCKET NUMBER: 27866/32168
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3519 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS

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; LOCATION: 52..3519
US-08-286-889-45
Alignment Scores:
Pred. No.: 1,29e-10 Length: 3519
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 9.61% Indels: 30
DB: 1 Gaps: 12

US-09-970-076-8 (1-333) x US-08-286-889-45 (1-3519)
QY 37 ProAlaCysTyrGly---GlyPheAspLeuTyrPheIleuAlaPheLysSerGlySerVal 55
DB 481 CCAAGATCCAGAGCAAGAAAGATGACATGCTTCTCGATGATGAGCTCCGAGCAATT 540
QY 56 ---LeuHisHisIleThrAsnGluIleTyrTyrPheValGluGlnLeuAlaHisIlePheIle 74
DB 541 GATCAAAAGTGAATTAACCAAGATGAAGAGCTTCGTCAAGCTTTGATGGGCAATGGCG 600
QY 75 SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThleuMetLys 94
DB 601 AGCAACACAGACCTGCTCCCTGATGCAATATCAACATCTGAGACTCATTTTACC 660
QY 95 LeuThrGluAspArg-----GluGlnIleArgGlnGlyLeuGlnGluLeu 109
DB 661 TTCACGGAAATTCAGAGACAGCTGAGCCCTGAGAGCTGGTGGATGCCATGCTCCAGCTC 720
QY 110 GlnLysValLeuProGlnGlyLysArgThrTyrMetHisGlnGlyPheGluArgAlaSerGlu 129
DB 721 CAA-----GGCTGACGTACACAGCTGCGGATGCCAAGAGTGTGA 765
QY 130 GlnIleTyrTyrGluAsnArgGlnIleTyrArgThrAla---SerValIleIleAlaLeu 148
DB 766 GAGCATTTTCATGACAGAAATGGGCGCCGAAAGAGTCCCAAGAAATCTAATGTCTATC 825
QY 149 ThrArgGlyGluLeuHisGluAspLeuPhePheTyrSerGlu-----ArgGluAlaAsn 166
DB 826 ACAGATGGGCAAAATTCAGAGACCCCTGGAGATATGACATGTCATCCCTGAGACAGAG 885
QY 167 ArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValLysAsp---PheAsnGlu 185
DB 886 AAAGCT-----GGATCATTTGCTATGCTATAGGGGTGGAGATGCTCCGGGAA 936
QY 186 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhe 199
DB 937 CCCACTGCCCTACAGAGACTGACACATGAGTGCATGCTCCCTGCGACAGACACGTGTC 996
QY 200 ProValAsnAspGlyPheGlnAlaLeuGlnGlnGlyIleIleHisSerIleLeuLysSer 219
DB 997 AAGGTGGGCAT---TTTGTAGCACTTCGACAGATCCAGCGCAAAATTCAGAGAAA--- 1050
QY 220 CysIleguIleLeuAlaAlaGluProSerThrIleCysAlaGlyLysSerPheGlnVal 239
DB 1051 -----ATCTTGGCATTTGAAGAACCAATCAAGTCAAGTCTTTCAGACAC 1101
QY 240 ValValaArgGlyAlaGlyPheArgHisAlaArgAsnValaAsp 253
DB 1102 GAGATGCACAAAGAGTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 4
US-08-485-618-45
; Sequence 45, Application US/08485618
; Patent No. 5728533
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
; STREET: 233 South Wacker Drive, 6300 Seear Tower

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? CITY : Chicago
? STATE : Illinois
? COUNTRY : United States
? ZIP : 60606-6402
? COMPUTER READABLE FORM:
? MEDIUM TYPE : Floppy disk
? OPERATING SYSTEM : PC-DOS/MS-DOS
? SOFTWARE : Patent Release #I.O., Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER : US/08/485,618
? FILING DATE:
? CLASSIFICATION : 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER : US 08/173,497
? FILING DATE : 23-DEC-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER : US 08/286,889
? FILING DATE : 5-AUG-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER : US 08/362,652
? FILING DATE : 21-DEC-1994
? ATTORNEY/AGENT INFORMATION:
? NAME : Williams Jr., Joseph A.
? REGISTRATION NUMBER : 38,659
? REFERENCE/DOCKET NUMBER : 27866/32797
? TELECOMMUNICATION INFORMATION:
? TELEPHONE : 312-474-6300
? TELEFAX : 312-474-0448
? TELEX : 25-3856
? INFORMATION FOR SEQ ID NO: 45:
? SEQUENCE CHARACTERISTICS:
? LENGTH : 3519 base pairs
? TYPE : nucleic acid
? STRANDEDNESS : single
? TOPOLOGY : linear
? MOLECULE TYPE : cDNA
? FEATURE:
? NAME/KEY : CDS
? LOCATION : 52..3519
US-08-485-618-45
Alignment Scores:
Pred. No.:      1.29e-10       Length:          3519
Score:         166.00        Matches:           66
Percent Similarity:    46.15%     Conservative:   42
Best Local Similarity:    28.21%     Mismatches:    96
Query Match:         9.61%       Indels:        30
                        Gaps:            12
DB:                1              12
US-09-970-076-8 (1-3513) x US-08-485-618-45 (1-3519)
Oy      ProbaCySeTyrgly---GlyPheApeLyuYrPhelileLeuaApLySerGIYSerVal 55
Db      CCAGAgCTGCACAGAACAAGATGAACATTGGTTCCTTGATTAAGTAGCGTCCGGAGCAATT 5400
Oy      56 ---leuHisieStrpaNgLuileTYrYPHeVaIgJungInLeuAliaHieLYpheIlle 74
Db      541 GATCAAAGTAGCATTACCAGCATGAAAGAGACTTCGTCCAAGCTTTGATGGGCCAGTTGCGG 6000
Oy      75 SerProclneuarNgetSetRphellelvalPhesertIrArngylThTheumElys 94
Db      601 AGCACCCAGCACTCGTTCTCCCTCGATGCAATCTCAAACATCTCGAMAGCACTATTACC 6608
Oy      95 LeuthrGlubapArg-----gJuIngIniIearNgInglyLeugluGluDen 109
Db      661 TTCACGGAAATTCAGAGCAAGCAAGCCTCAAGCCTCGATGAGATGCATGCTCCACAGCTC 7200
Oy      110 GlInlySalluePrroglYgiYaEPTrTYrmEthIsagInglyPheguARgalaserglu 129
Db      721 CAAd-----ggcctGaGstrAcacaggccctggcgatncagaMaagtgttAAA 7655
Oy      130 GlmIEryTYrgLUenarNgInglyTYrArghrrala--ServalliElalDeu 148
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Db      766 GAGCATTTCTCTACCAAGATGGGGCCCCGAAAAAGTCCCAAGAGATACTAAATTGTCTATC 825
      149 ThrApGgluLeuWhIsgluApRLeuPhePheTySerglu-----ArgGluAlaApn 166
      826 ACAATAGGGCGAATTCAGAGACCCCTGGAGTATGACATGTCTATCCCTCGAAGCAGAG 885
      167 ArgSerxArgAerLeuGluYalaIleValTyTyrCysValGluValuVaaP---PheaSngu 185
      886 AAACT-----GGATCATTCGGCTATGCTATGAGGGGTGGAGAGATGCTTCGGGAA 936
      186 ---ThrgInLeuAlaArgIle-----AlaApSerTyvAaPheValPhe 199
      937 CCCATGCCCCCTACAGAGAGCTGAACACCATTTGGCTCACTCCCTCGCAGACCACTGTTC 996
      200 ProValaSnApRgLyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuYalYasEr 219
      997 AAGGTGGGCAAT---TTGTGTGCACTTCGCAGCATCCAGCGCGCAAAATTCAGAGAAA--- 1050
      220 CysIleGluIleLeuAlaIaIaGluProSerThrIleCysAlaGlyGluSerPheGlnVal 239
      1051 -----ACCTTTGGCATTTGAAAGGAACCGAATCAAGGCTCAAGTACTTCTTTCAGCAC 1101
      240 ValValARgGlyAaNGlyPheArgHisAlaArgAaValaAP 253
      1102 GAGATGTCACAGAAAGTTTTCAGCTCAGCTCTCTCAATGAT 1143

RESULT 5
/ Sequence 45, Application US/08362652
/ Patent No. 5766850
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, W. Michael
/ APPLICANT: Van der Vlieten, Monica
/ TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
/ NUMBER OF SEQUENCES: 93
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerststein, Murray & Borun
/ STREET: 233 South Wacker Drive, 6300 Seair Tower
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States
/ ZIP: 60606-6402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/362,652
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/173,497
/ FILING DATE: 23-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/286,889
/ FILING DATE: 5-AUG-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27866/32391
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 45:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3519 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA

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Oy      130 GlnIleuTgUgUaAmAaNgInleYrUaNgThIaA---SeVaIleleuAleu 148
Db      766 GAGCATTTTCATGAGAAATGGGGCCCGAAAAGATGCCAAGAAATCTAATTTCATG 825
Oy      149 ThIAeRgIglUeUleAglUaRleuPheRheTySeRgIU----ArgIUaUlaaV 166
Db      826 ACAATGGGAGAAATTCAGAGACCCCTGGAGTATGACATGTGATCCCTGAAAGCAG 885
Oy      167 ArgSeRlaRgaRleuGlyUaIaIleValIyTcYvaIaGlyUaR---PheaNgIU 185
Db      886 AAAGCT-----GGAGATCATTCGATGCTAATAGGGAGTGGAGATCGCTCCGGAA 936
Oy      186 ---ThgIUleUlaARgIle-----AlaepSeRlyAspH:vaIaPhe 199
Db      937 CCCACTGCCCTCAAGAGCTGAACCACTGGCTAGCTCCCTCCAGAGAACCACTGTC 996
Oy      200 ProValaenAeRgIyPheGInaIaLeuGInglYleIleH:aseRleUeUlySeR 219
Db      997 AAGGTGGGCAT---TTTGTGCACTTTCGACAGATCCAGCGCAATTCAGAGAA--- 1050
Oy      220 CysIleGluIleUeUaIaAlaGInUProSeRThrIleCyvaIaGlyGluSeRheGInVaI 239
Db      1051 -----ATCTTGGCCATGGAAGAAACCGAATCAAGGTCAAGATGCTCTTCAGCAC 1101
Oy      240 ValValaRgIyAeNgIyPheRgHIsIaAaNgAenValaep 253
Db      1102 GAGATGTCAAGAGAGTTTTCAGCTCAGCTCTCTCAATGGAT 1143

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01 130 GlnIleYrYrYrGluAsnArgGlnIleYrYrArgThrAla---SerValIleIleAlaIleu 148
02 149 ThrArgGluYrYrLeuHieGluAspLeuPhePheYrSerGlu-----ArgGluAlaAsn 166
03 826 ACAAGTGGGCAAGAAATTCAGACGACCCCTGGAGGTATTAACATGTTCATCCCTGAAGCAGAG 885
04 167 ArgSerArgAspLeuGluYrAlaIleValYrYrCysValGluValYrAsp--PheAsnGlu 185
05 886 AAAGCT-----GGGATCATCTGGCTATGCTATAGGGGTGGAGATGCCCTCCGGGAA 936
06 186 ---ThrGlnAlaAlaArgIle-----AlaAspSerLysAspHisValPhe 199
07 937 CCCATGCCCTACAGACCTGAACACCATTTGGCTCAGCTCCCTGCAGAGACCATGTGTC 996
08 200 ProValAsnArgGluPheGlnAlaLeuGlnGluIleIleHisSerIleLeuYrYrSer 219
09 997 AAGGTGGGCAT---TTGTAGCACTTGGCAGACATCCAGCGCAATTCAGAGAA--- 1055
10 220 CysIleGluIleLeuAlaGluPheSerThrIleCysAlaGluYrSerPheGlnVal 239
11 1051 -----ATCTTGCCATTTGAAGAAACCGAATCAAGTCAAGTAGTTCCTTCAGACAC 1101
12 240 ValValArgGluYrAsnGluPheArgHisAlaArgAsnValAsp 253
13 1102 GAGATGTCAACAAGAGTTTACGTACGCTCTCTCAATGAT 1143
14
15 RESULT 7
16 US-08-482-293A-45
17 Sequence 45, Application US/08482293A
18 Patent No. 5831029
19 GENERAL INFORMATION:
20 APPLICANT: Gallatin, W. Michael
21 APPLICANT: Van der Vieren, Monica
22 TITLE OF INVENTION: No. 5831029e1 Human 2 Integrin Alpha Subunit
23 NUMBER OF SEQUENCES: 103
24 CORRESPONDENCE ADDRESS:
25 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
26 STREET: 233 South Wacker Drive, 6300 Sear Tower
27 CITY: Chicago
28 STATE: Illinois
29 COUNTRY: United States
30 ZIP: 60606-6402
31 COMPUTER READABLE FORM:
32 MEDIUM TYPE: Floppy disk
33 COMPUTER: IBM PC compatible
34 OPERATING SYSTEM: PC-DOS/MS-DOS
35 SOFTWARE: PatentIn Release #1.0, Version #1.25
36 CURRENT APPLICATION DATA:
37 APPLICATION NUMBER: US/08/482,293A
38 FILING DATE:
39 CLASSIFICATION: 530
40 PRIOR APPLICATION DATA:
41 APPLICATION NUMBER: US 08/173,497
42 FILING DATE: 23-DEC-1993
43 PRIOR APPLICATION DATA:
44 APPLICATION NUMBER: US 08/286,889
45 FILING DATE: 5-AUG-1994
46 PRIOR APPLICATION DATA:
47 APPLICATION NUMBER: US 08/362,652
48 FILING DATE: 21-DEC-1994
49 ATTORNEY/AGENT INFORMATION:
50 NAME: Williams Jr., Joseph A.
51 REGISTRATION NUMBER: 38,659
52 REFERENCE/DOCKET NUMBER: 27866/32684
53 TELECOMMUNICATION INFORMATION:
54 TELEPHONE: 312-474-6300
55 TELEFAX: 312-474-0448
56 TELEX: 25-3856
57 INFORMATION FOR SEQ ID NO: 45:
58 SEQUENCE CHARACTERISTICS:

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APPLICANT: Gallatin, W. Michael  
APPLICANT: Van der Vieren, Monica  
TITLE OF INVENTION: No. 58374781 Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Sear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,363  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3519 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 52..3519  
US-08-943-363-45  
Alignment Scores:  
Pred. No.: 1,296-10 Length: 3519  
Score: 166.00 Matches: 66  
Percent Similarity: 46.15% Conservative: 42  
Best Local Similarity: 28.21% Mismatches: 96  
Query Match: 9.61% Indels: 30  
DB: 2 Gaps: 12  
US-09-970-076-8 (1-333) x US-08-943-363-45 (1-3519)  
QY 37 ProAlaCybTYrGLY---GLYpheaSpLeuTYrPheileLeuApLyseScLySeArV 55  
DB 481 CCAAGGTGTCCAGGACAGAGATGACATGCTTCCCTGATGATGCGCTCCGCGACGATT 540  
QY 56 ---LeuHlNHlSTpAbnGlnLleTYrTYrPheValGlnGlnLeuAlNHlLeYpBheile 74  
DB 541 GATCAAGTGAATTACCAAGATGAAAGACTTCGTCAAAGCTTTGATGGCGCAGTTGGCG 600  
QY 75 SerPpOGlnLeuArXmetSerPheileValPheSerThrArGlyThrThrLeuMetLys 94  
DB 601 AGCACCAGACCTCTTCTCCCTGATGCAATCTCAACATCTTGAAGACTTATTATTC 660  
QY 95 LeuThrgLluAspArg-----GluGlnIleArGlnGlnIYleuGlnLluLeu 109

DB 661 TTCAAGAAATTCAGAGACGCTGAGCCCTGACAGCTGTGTGATGCCATGCTCCAGCTC 720  
QY 110 GlnYsValLeuPpOGlyGLYAspPhrTYrMetHISGlnGlnPheGluArGAlaSerGlu 129  
DB 721 CAA-----GSCCTGCGTACAGAGCTCGGGGATCCAGAAAGTGCTGAA 765  
QY 130 GlnIleTYrTYrGluAsnArGlnGlnIYrArGrThraLl-----SerValIleLeuAla 148  
DB 766 GAGCATTTCAATACAGAAATGCGGCGCCGAAAAGTGCCAGAAAGATCTAATTCATC 825  
QY 149 ThrAspGlyGluLeuHISGluAspLeuPheTYrSerGlu-----ArgGluAlaAsn 166  
DB 826 ACAGATGGGCAAAATTCAGAGACCCCTGAGATACATATGTCATCCCTGAAGCAGAG 885  
QY 167 ArgSerArGAspLeuGlyAlaIleValTYrCySValGlyValYAsp---PheAsnGlu 185  
DB 886 AAAGCT-----GGATCATTCGCTATCTATAGGGGGGAGATGCTTCGGGAA 936  
QY 186 ---ThrgInLeuAlaArgIle-----AlaAspSerLYAspHISValPhe 199  
DB 937 CCCACTGCCCTACAGAGACTGAACACCATTTGGCTCAGCTCCCTCGACAGACCACTGTC 996  
QY 200 ProValAsnAspGlyPheGlnAlaLeuGlnGlnIYleIleHISerIleLeuLYsSer 219  
DB 997 AAGTGGGCAAT---TTGTAGCACTTCGACAGATCCAGCGCAAAATTCAGAGAAA--- 1050  
QY 220 CysIleGlnIleLeuAlaAlaGluPpSerThrIleCYsAlaGlyLysSerPheGlnVal 239  
DB 1051 -----ATCTTTCATTTGAAGAAACCAATCAAGCTCAAGTAGTCTTTCAGCAGC 1101  
QY 240 ValValArGlyAsnGlyPheArGHisAlaArGAsnValAsp 253  
DB 1102 GAGATGTCAAGAAAGTTTCAGCTCAGCTCTCTCAATGAT 1143  
RESULT 9  
US-09-193-043-45  
Sequence 45, Application US/09193043  
Patent No. 6251395  
GENERAL INFORMATION:  
APPLICANT: Gallatin, Michael W.  
APPLICANT: Van der Vieren, Monica  
TITLE OF INVENTION: No. 6251395e1 Human 2  
FILE REFERENCE: 27866/35004  
CURRENT APPLICATION NUMBER: US/09/193,043  
CURRENT FILING DATE: 1998-11-16  
EARLIER APPLICATION NUMBER: 08/173,497  
EARLIER FILING DATE: 1993-12-23  
EARLIER APPLICATION NUMBER: 08/286,889  
EARLIER FILING DATE: 1994-08-05  
EARLIER APPLICATION NUMBER: 08/362,652  
EARLIER FILING DATE: 1994-12-21  
EARLIER APPLICATION NUMBER: 08/943,363  
EARLIER FILING DATE: 1997-10-03  
NUMBER OF SEQ ID NOS: 114  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 45  
LENGTH: 3519  
TYPE: DNA  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (52)..(3516)  
OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-193-043-45  
Alignment Scores:  
Pred. No.: 1,296-10 Length: 3519  
Score: 166.00 Matches: 66  
Percent Similarity: 46.15% Conservative: 42  
Best Local Similarity: 28.21% Mismatches: 96  
Query Match: 9.61% Indels: 30  
DB: 3 Gaps: 12





Score:	166.00	Matches:	66
Percent Similarity:	46.15%	Conservative:	422
Best Local Similarity:	28.21%	Mismatch:	96
Query Match:	9.61%	Indels:	30
DB:	1	Gaps:	12

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US-09-970-076-8 (1-333) x US-08-485-618-52 (1-3803)
Oy      37 ProAlaCyEUTGly----GlyPheAerLeuTyrPheIleLeuArbrySerGIyserval 55
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      430 CCAAGCTGCCAGACAAAGATGAAGCATTTGGCTTTCTTAATTGATGGCTCCGGACATC 489
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy      56 ---LeuNIhNtErDraVnGluiLeTyrTyCPheValGIuGlInLeuAlaNiShyRPhelle 74
        :::: |:::: |:::: |:::: |:::: |:::: |:::: |:::: |::::
Db      490 GATCAAAGTACTTTAACCSAGATGAAGAAGCATTCGTAAAGCTTTGATGGCGGCATTTGGCG 549
        ::: |:::: |:::: |:::: |:::: |:::: |:::: |:::: |::::
Oy      75 SerProGlInLeuArXmeSerPheilevalPheSerThraGlyLThrTriueMetLyv 94
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      550 AGCACACAGACACCTCGTTCTCCCTGATGCAATCTCAAAATCCTGAAAGACTCATTTTACC 609
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy      95 LeuthrGuArbArg-----GluGlInIeaGrInlYeuGlInuGlInu 109
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      610 TTCAAGGAATTCAGAGACAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 669
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy      110 GlInyValLeuProGIyGIyArbTrhTYrMeNIeGlIGlyPheGIuArbAlaseGln 129
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      670 CAAT-----GGCTGAGCTGACAGAGCTGGGAGTATCAGAAAGTGCGMAA 714
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy      130 GlInIeTYrTYrGIuArbArGlnGlnIyTYrArGThrala--SerValIleIealaleu 148
        :::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      715 GAGCTATTTCATAGAGCAAGATGGGGCCGAAAAGTGGCCAGAAAGATCAATATTCATC 774
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy      149 ThrArbRGlyGIuLeuNIhNtErDraVnLeuPheRheTYrSerGIu----ArgGIuAlaan 166
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      775 ACAGATGGGACAGAAATTCAGAGACCCCCCTGAGATRAAGACAATGTATCCCTTGAGAGAGAG 834
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy      167 ArgSerArGArbRleuGIyAlaIleValTYrCySvaGIyValLyvAr--PheanGln 185
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      835 AAAGCT-----GGAGTATTCGCTATGGCTATAGGGGTGGAGATGCTTCGGGAA 885
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy      186 ---ThrGIuLeuAlaArgIle-----AlaArbSerLYuArbRIeValPhe 199
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      886 CCCATGCGCTTACAGAGCTGAACAACATTTGCTGAGCTCCCTCCGAGAGACCATGTTC 945
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy      200 ProValaaArbRGlyPheGlInIaLeuGlnGlnIyIeNIhISerIIeLeuLybryser 219
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      946 AAGGTGGGCAT---TTTGACACTTTCGACAGATCAAGCGCAAAATTCAGAGAAA--- 999
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy      220 CyvIleGIuIleLeuAlaIaGIuProSerthrIleCyAlaGIyLyuSerPheGlnVal 239
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1000 -----ATCTTGCCATTTGAAGGAACGAAATCAAGGTCAAGTAGTTCCTTTCAAGAC 105
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy      240 ValValaRgGIyAaNGlyPheArGhNIbAlaArGaVnaIaAr 253
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1051 GAGATGTCAAGAAAGTTTCAGCTCAGCTCTCTCATAGAT 1092
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
US-08-362-652-52
; Sequence 52, Application US/08362652
; Patent No. 5766850
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
; COMPUTER READABLE FORM:
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: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/362,652
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/173,497
: FILING DATE: 23-DEC-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/286,889
: FILING DATE: 5-AUG-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Williams Jr., Joseph A.
: REGISTRATION NUMBER: 38,659
: REFERENCE/DOCKET NUMBER: 27866/32391
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-474-6300
: TELEFAX: 312-474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 52:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3803 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..3486
: US-08-362-652-52

Alignment Scores:
Pred. No.: 1,47e-10 Length: 3803
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 9.61% Indels: 30
Gaps: 12
DB: 1

US-09-970-076-8 (1-333) x US-08-362-652-52 (1-3803)
QY 37 ProAlaCyseTyrgLy---gLyPheAspLeuTrpPheIleLeuApLySerGlySerVal 55
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 430 CCAAGAGTGTCCAGACAAAGATGAAGATGCATTGGCTTTCTCGATTGATGCTGCCGACGATT 489
QY 56 ---LeuHHisHTripAsnGlnUilerTyTrpHeValGlutInLysuaAHslySPhelIe 74
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 490 GATCAAAGTGACTTTAACCAGATGAAGCATTCGTCAAAAGCTTGAAATGAGCAGATTGGCG 549
QY 75 SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrTrpLeuMetLys 94
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 550 AGCACCAAGACCTCGTTCTCTCTGTATGCAATACATAACAATCTGAAAGACTATTTAACC 609
QY 95 LeuThrGluAspArg-----GluGlnIleaArgGlnGlyLeuGlnGluLeu 109
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 610 TTACCGGAATTCAGAAGCAGCGCTGAGCGCTCAGAGCGCTGGTAGATGCATGCTCCAGACTC 665
QY 110 GlnLysValLeuProGlyGlyAspThrTyTrpMetHisGlnGlyPheGluArgLaSerGlu 129
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 670 CAA-----GGCCTGACGrAACACAGCGCTCGGGCATCCAGAAAAGTGATGAAA 714
QY 130 GlnIleTyTrpGlnAsnArgGlnGlyTyArgThrAla---SerValIleIleIleLys 148
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 715 GAGCTATTTTCATATGACAAAGATGGGGCCGAAAAAGTGCCAAGAAAGATATATATGTCATC 774
QY 149 ThrAspGlyGlnLeuHisGlnLysPheLeuPhePheTyTrpSerGlu-----ArgGluAlaAsn 166
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 775 ACAAGATGGGCAAGAAATTCAGAGACCCCCCTGGAGATrTAAGACATGTCATCCCTGAAGCGAG 834
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 167 ArgSerArgAspLeuGlyAlaIleValTyrcyBValGlyValLysaaP---PheAsnGlu 185

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Db      835 AAGCT-----GGGATCATGCTATAGGGGTGAGATGCCCTCCGGAA 885
Qy      186 ---ThrGlnLeuAlaArgIle-----AlaAspSerLeuAspHisValPhe 199
Db      886 CCCACTGCCCTTACAGAGCTGAACACATTGGCTCAGCTCCCTCCAGAGACACAGTTC 945
Qy      200 ProValaAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuValysSer 219
Db      946 AAGGTGGGCAT---TTTGTAGCACTTCCAGACATCCACGGCAATTCCAGAGAAA--- 999
Qy      220 CysIleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnVal 239
Db      1000 -----ATCTTGCCATTGAAAGAACCGAATCAAGGTCAAGTATCTTCCAGCAC 1050
Qy      240 ValValaArgGlyAsnGlyPheArgHisAlaIaArgAsnValaAsp 253
Db      1051 GAGATGTCACAAAGAGTTTCAGCTCAGCTCTCTCAATGAGAT 1092

```

## RESULT 14

US-08-605-672-52

Sequence 52, Application US/08605672

Patent No. 5817515

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael

APPLICANT: Van der Vieren, Monica

TITLE OF INVENTION: NO. 5817515el Human 2 Integrin Alpha Subunit

NUMBER OF SEQUENCES: 103

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &amp; Borun

STREET: 233 South Wacker Drive, 6300 Sear Tower

CITY: Chicago

STATE: Illinois

COUNTRY: United States

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/605,672

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/362,652

FILING DATE: 21-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 27866/32684

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:

LENGTH: 3803 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..3486

US-08-605-672-52

```

Alignment Scores:
Pred. No.: 1.47e-10 Length: 3803
Score: 166.00 Matches: 66
Percent Similarity: 46.15% Conservative: 42
Best Local Similarity: 28.21% Mismatches: 96
Query Match: 9.61% Indels: 30
DB: 1 Gaps: 12

```

US-09-970-076-8 (1-333) x US-08-605-672-52 (1-3803)

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Qy      37 ProAlaCysTyrGly---GlyPheAspLeuTyrPheIleLeuAspLysSerGlySerVal 55
Db      430 CCAGAGTTCACAGGACAAAGATGAGCATTTCTTCCATGATGATGCTCCGGCGAGCAT 489
Qy      56 ---LeuHisIleTPAsnGluIleTyrTyrPheValGluGlnLeuAlaHisIlePheIle 74
Db      490 GATCAAACTGACTTTTACCAAGATGAAGAGCTTCGCAAGCTTTGATGGCCAGTTGGCG 549
Qy      75 SerProGlnLeuAArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys 94
Db      550 AGCAGCAGCACCCTGCTTCCCTGATGCAATCATCAATCAATCCGAAAGATCTATTAC 609
Qy      95 LeuThrgIuAspArg-----GluGlnIleArgGlnGlyLeuGlnGluLeu 109
Db      610 TTCACGGAATTCAGAGACAGCAGCTGAGCCCTGAGAGCTGTGGATGCCATGTCAGCTC 669
Qy      110 GlnIysValLeuProGlyGlyAspThrTyrMetHisGluGlnGluPheGluArgAlaSerGlu 129
Db      670 CAA-----GGCCTGACGTACACAGCTCCGGGATCCAGAAAGGTGGTGA 714
Qy      130 GlnIleTyrGlnIuAsnArgGlnGlyTyrArgThrAla---SerValIleIleAlaLeu 148
Db      715 GAGCTATTTCATACAGAAATGAGGAGCCGGAAGAGTCCGAAGAAATCTAATTCATC 774
Qy      149 ThrAspGlyGluLeuHisGluAspLeuPhePheTyrSerGlu---ArgGlnAlaAsn 166
Db      775 ACAAGTGGGCAAAATTCAGAGACCCCTGAGATATACATGCATCCATCGAAGACAG 834
Qy      167 ArgSerArgAspLeuGlyAlaIleValTyrCysValGlyValLysAsp---PheAsnIu 185
Db      835 AAGCT-----GGGATCATGCTATAGGGGTGAGATGCCCTCCGGAA 885
Qy      186 ---ThrGlnLeuAlaArgIle-----AlaAspSerLeuAspHisValPhe 199
Db      886 CCCACTGCCCTTACAGAGCTGAACACATTGGCTCAGCTCCCTCCAGAGACACAGTTC 945
Qy      200 ProValaAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuValysSer 219
Db      946 AAGGTGGGCAT---TTTGTAGCACTTCCAGACATCCACGGCAATTCCAGAGAAA--- 999
Qy      220 CysIleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnVal 239
Db      1000 -----ATCTTGCCATTGAAAGAACCGAATCAAGGTCAAGTATCTTCCAGCAC 1050
Qy      240 ValValaArgGlyAsnGlyPheArgHisAlaIaArgAsnValaAsp 253
Db      1051 GAGATGTCACAAAGAGTTTCAGCTCAGCTCTCTCAATGAGAT 1092

RESULT 15
US-08-482-293A-52
Sequence 52, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States

```

ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,293A  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/362,652  
FILING DATE: 21-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: William J., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/32684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3803 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..3486  
US-08-482-293A-52  
  
Alignment Scores:  
Pred. No.: 1.47e-10 Length: 3803  
Score: 166.00 Matches: 66  
Percent Similarity: 46.15% Conservative: 42  
Best Local Similarity: 28.21% Mismatches: 96  
Query Match: 9.61% Indels: 30  
DB: 2 Gaps: 12  
  
US-09-970-076-8 (1-333) x US-08-482-293A-52 (1-3803)  
QY 37 ProAlaCybTyrgLy---GlyPheAspLeuTyrrPheIleuAspLysSerGlySerVal 55  
DB 430 CCAGAGTGTCCAGAGCAAGATGAGCATGTGCTTCCGATGATGCGTCCGCGACGATT 489  
QY 56 ---LeuHisIstPAsngIuIeTyrrTyrrPheValGluGlnLeuAlaHisLysPheIle 74  
DB 490 GATCAAGTGACTTATCCAGATGAGGAGCTTCGTCAGAACTTGAATGCGCCAGTGGCG 549  
QY 75 SerProGlnLeuArgMetSerPheIleValPheSerThrArgGlyThrThrLeuMetLys 94  
DB 550 AGCACCGACACCTGCTTCTCCCTGATGCATATCTCAACATCTCGAAGATCATTTTACC 609  
QY 95 LeuThrGlnAspArg-----GluGlnIleArgGlnGlyLeuGluGluLeu 109  
DB 610 TTCACGGATTCAGAGCAGCGCTGAGCCCTCAGAGCCTGGGATGCCATGCTCCAGCTC 669  
QY 110 GlnLysValLeuProGlyGlyAspThrTyrrMetHisGluGlyPheGluArgAlaSerGlu 129  
DB 670 CAA-----GGCCTGACGTACACAGCCTCGGCGATCCAGAAAGTGTGAA 714  
QY 130 GlnIleTyrrTyrrGluAsnArgGlnGlyTyrrArgThrAla---SerValIleIleAlaLeu 148  
DB 715 GAGCATTTTCATACAGAAATGGGGCCCGCAAAAGTCCAAAGAAATATTAATTGTATC 774

QY 149 ThrAspGlyGluLeuHisGluAspLeuPhePheTyrrSerGlu-----ArgGluAlaAsn 166  
DB 775 ACAGATGGCAGAAATTACAGAGACCCCTGGAGTATGACATGTCATCCCTGAAGCAGAG 834  
QY 167 ArgSerArgAspLeuGlyAlaIleValTyrrCysValGlyValLysAsp---PheAsnGlu 185  
DB 835 AAAGCT-----GGGATCATTCGCTATGCTATAGGGGTGGAGATGCTTCGGGAA 885  
QY 186 ---ThrGlnLeuAlaArgIle-----AlaAspSerLysAspHisValPhe 199  
DB 886 CCACATCCCTTACAGAGAGCTGAACACACCATTTGGCTCAGCTCCCTCGCAGACACGATTC 945  
QY 200 ProValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleHisSerIleLeuLysSer 219  
DB 946 AAGTGGGCAAT---TTTGTAGCATTCCGACATCCAGCGCGCAAAATTTCAGAGAAA--- 999  
QY 220 CysIleGluIleLeuAlaIleGluProSerThrIleCysValaGlyGluSerPheGlnVal 239  
DB 1000 -----ATCTTGGCATTTGAAGAACCAATTCAGAGTCMAAGTACTTCTTCACACAC 1050  
QY 240 ValValArgGlyAsnGlyPheArgHisAlaArgAsnValAsp 253  
DB 1051 GAGATGTACAGAAAGGTTTCAGCTCAGCTCTCTCAATGAT 1092

Search completed: June 22, 2004, 02:55:01  
Job time : 87.528 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Run on: June 22, 2004, 01:18:40 ; Search time 122.84 Seconds

(without alignment)  
2547.963 Million cell updates/sec

Title: US-09-970-076-6

Sequence: 1 MATNRALAGTGFQWLSLAT.....QAPPNRAPPPRRPPRSV 564

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=MINAM62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptio -NOR=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09970076 -CGN\_1\_1\_148@runat\_21062004\_125531\_8763 -NCPU=6 -ICPU=3  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

Issued\_Patents\_NA:\*  
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4: /cg2\_6/ptodata/2/1na/6B.COMB.seq:\*  
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6: /cg2\_6/ptodata/2/1na/Backfillseq1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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	2	1392	46.0	1609	4	US-09-620-312D-8		Sequence 8, Appl1
	3	213	7.0	318	3	US-09-165-264-12		Sequence 12, Appl1
	4	213	7.0	320	3	US-09-165-264-14		Sequence 14, Appl1
	5	208	6.9	320	3	US-09-165-264-13		Sequence 13, Appl1
	6	206	6.8	320	3	US-09-165-264-7		Sequence 7, Appl1
	7	205.5	6.8	51259	3	US-08-781-891-209		Sequence 209, App
	8	205.5	6.8	51259	4	US-09-618-166-209		Sequence 209, App
	9	205	6.8	320	3	US-09-165-264-11		Sequence 11, Appl1
	10	203	6.7	319	3	US-09-165-264-8		Sequence 8, Appl1
	11	199.5	6.6	324	4	US-09-547-693-234		Sequence 234, App
	12	199	6.6	53577	3	US-08-658-136-1		Sequence 1, Appl1

13	195	6.4	16442	3	US-08-781-891-208	Sequence 208, App
14	195	6.4	16442	4	US-09-618-166-208	Sequence 208, App
15	194	6.4	53526	3	US-08-658-136-2	Sequence 2, Appl1
16	192	6.3	43280	2	US-08-804-227C-1	Sequence 1, Appl1
17	191.5	6.3	2230	1	US-08-217-327-5	Sequence 5, Appl1
18	189.5	6.3	1926	4	US-09-249-565A-2	Sequence 2, Appl1
19	189.5	6.3	1926	4	US-09-410-399-3	Sequence 3, Appl1
20	189.5	6.3	2580	4	US-09-050-863-2	Sequence 2, Appl1
21	189.5	6.3	2580	4	US-09-359-081-2	Sequence 1, Appl1
22	189.5	6.3	5452	2	US-09-130-114-1	Sequence 14, Appl1
23	189.5	6.3	8705	4	US-09-647-344A-14	Sequence 1, Appl1
24	189.5	6.3	9600	4	US-08-910-647-1	Sequence 1, Appl1
25	189.5	6.3	9600	4	US-09-620-925-1	Sequence 1, Appl1
26	189.5	6.3	10596	1	US-07-884-811-15	Sequence 15, Appl1
27	189.5	6.3	10596	1	US-07-884-811-15	Sequence 15, Appl1
28	189.5	6.3	10596	1	US-08-087-783A-15	Sequence 15, Appl1
29	189.5	6.3	10596	2	US-08-194-088B-15	Sequence 15, Appl1
30	189.5	6.3	10596	2	US-08-194-087-15	Sequence 15, Appl1
31	189.5	6.3	10596	2	PCT-US93-04648-15	Sequence 15, Appl1
32	189.5	6.3	12001	1	US-08-458-568A-11	Sequence 11, Appl1
33	189.5	6.3	16080	4	US-09-724-566A-48	Sequence 48, Appl1
34	187.5	6.2	925	3	US-08-836-003-1	Sequence 1, Appl1
35	187.5	6.2	925	3	US-09-078-166-1	Sequence 1, Appl1
36	187.5	6.2	925	3	US-08-997-467-1	Sequence 1, Appl1
37	187	6.2	4403765	3	US-09-103-840A-2	Sequence 2, Appl1
38	187	6.2	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
39	186.5	6.2	3196	4	US-09-704-449-1	Sequence 1, Appl1
40	186.5	6.2	152331	3	US-09-128-155-16	Sequence 16, Appl1
41	186	6.1	246	4	US-09-547-693-232	Sequence 232, App
42	186	6.1	913	1	US-08-217-327-3	Sequence 3, Appl1
43	186	6.1	913	1	US-07-885-970A-3	Sequence 3, Appl1
44	186	6.1	913	1	US-08-298-687A-3	Sequence 3, Appl1
45	186	6.1	913	1	US-08-530-797-2	Sequence 2, Appl1

## ALIGNMENTS

## RESULT 1

US-09-833-381-998  
Sequence 998, Application US/09833381  
Patent No. 6672186  
GENERAL INFORMATION:  
APPLICANT: Robison, Keith E.  
TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs  
FILE REFERENCE: 5800-119  
CURRENT APPLICATION NUMBER: US/09/833,381  
CURRENT FILING DATE: 2001-04-11  
PRIOR APPLICATION NUMBER: 09/516,448  
PRIOR FILING DATE: 2000-02-29  
NUMBER OF SEQ ID NOS: 2050  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 998  
LENGTH: 2459  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1) ... (2459)  
OTHER INFORMATION: n = A,T,C or G  
US-09-833-381-998

## Alignment Scores:

Pred. No.:	5.18e-116	Length:	2459
Score:	1650.00	Matches:	365
Percent Similarity:	65.98%	Conservative:	21
Best Local Similarity:	62.39%	Mismatches:	76
Query Match:	54.55%	Indels:	124
DB:	4	Gaps:	12

US-09-970-076-6 (1-564) x US-09-833-381-998 (1-2459)

QY 1 Metatrralagtlargaralabengllyllleglphneglntrrpleusertleu1lanthr 20

[illegible]

QY	380	AlasertYrYrYrGlyGlyArgGlyValGlyGlyLysAlaArgMetGluValAlaGTrpGly	399
Db	1459	-----GGG	1461
QY	400	GluYrGlySerThrGluGluGlyAlaLysLeuGluYrValAlaYsAsnAlaArgValLys	419
Db	1462	GAGAGAGA-----GCCAAACATGCTGGTTTACA	1491
QY	420	Met-----ProGluGluYrGluPheProGlu	429
Db	1492	CTTTCCTATTATTACGATGATGAGGGCAGAGACAGCCCTGGAGTTACGACACTGAG	1551
QY	430	ProArgLeuLeuAsnAsnMetArgArpProSerSerProArgLysTrpTyrSerPro	449
Db	1552	TGCCCAACATGAGAAACATCAGAGG-----GACAGGAACG-TTCCCTCT	1601
QY	450	-----LelyGlyLysLeuAspAlaLeuTrpValLeu	461
Db	1602	TAACCAACAGTTTCAAGACCTTACTGGAGGCACTTATGGCTACATTAATCACTCCATG	1661
QY	462	ArgLysGlyTyrAspArgValSerValMetArgProGluTrpGly-----AspThr	478
Db	1662	CGGTGGGCATCAGCAGCATCTGCTGCAGACCCAACTTTGAGGTGAGATTTCACAGT	1721
QY	479	GlyArgCysIleAsnPheThrArgValLysAsnAsnGluProAlaLysTyrProLeuAsn	498
Db	1722	TTCTTTATTATTGAACTTCCCCAGAGCTCCCACTAATTCCTCCATCTAT-----	1772
QY	499	AsnAlaTyrHisIleHisSerSerProProAlaProIle-----	511
Db	1773	-----CTCTCTCCCTTTCCCAAAAGAAAAGAGAGCAG	1811
QY	512	-----TyrThrPro	514
Db	1812	CAGTGTGGATACCGTATCATCCAGAGCCTGTTCTCTCCCATTAATAGGCAAAACAGC	1871
QY	515	ProProProAlaProHisCysProProProPro-----ProSerAlaProThr	530
Db	1872	CCTGGCAAGATATTTCCTACTCCCGGCCCATGTCAGTAAATAATCCAAAATTGCTATA	1931
QY	531	ProProIleProSer	535
Db	1932	TTCCACCTGCCAAGC	1946

RESULT 2  
 US-09-620-312D-8  
 / Sequence 8, Application US/09620312D  
 / Patent No. 6569662  
 / GENERAL INFORMATION:  
 / APPLICANT: Tang, Y. Tom  
 / APPLICANT: Liu, Chenghua  
 / APPLICANT: Asundi, Vinod  
 / APPLICANT: Zhang, Jie  
 / APPLICANT: Ren, Feiyan  
 / APPLICANT: Chen, Rui-hong  
 / APPLICANT: Zhao, Qing A.  
 / APPLICANT: Wehman, Tom  
 / APPLICANT: Xue, Aidong J.  
 / APPLICANT: Yang, Yonghong  
 / APPLICANT: Wang, Jiah-Rui  
 / APPLICANT: Zhou, Ping  
 / APPLICANT: Ma, Yunding  
 / APPLICANT: Wang, Dunrui  
 / APPLICANT: Wang, Zhiwei  
 / APPLICANT: John Tillinghast  
 / APPLICANT: Drmanac, Radoje T.  
 / TITLE OF INVENTION: No. 656962e1 Nucleic Acids and  
 / FILE REFERENCE: Polypeptides  
 / CURRENT APPLICATION NUMBER: US/09/620,312D  
 / CURRENT FILING DATE: 2000-07-19  
 / PRIOR APPLICATION NUMBER: 09/552,317

```

/ RESULT 2
/ US-09-620-312D-8
/ Sequence 8, Application US/09620312D
/ Patent No. 6569662
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Zhang, Jie
/ APPLICANT: Ren, Feiyan
/ APPLICANT: Chen, Rui-hong
/ APPLICANT: Zhao, Qing A.
/ APPLICANT: Weinman, Tom
/ APPLICANT: Xue, Aldong J.
/ APPLICANT: Yang, Yonghong
/ APPLICANT: Wang, Jian-Rui
/ APPLICANT: Zhou, Ping
/ APPLICANT: Ma, Yungqing
/ APPLICANT: Wang, Dunxui
/ APPLICANT: Wang, Zhiwei
/ APPLICANT: John Tillinphast
/ APPLICANT: Drmanac, Radoje T.
/ TITLE OF INVENTION: NO. 6569662e1 Nucleic Acids and
/ FILE OF INVENTION: Polypeptides
/ FILE REFERENCE: 784CIP28
/ CURRENT APPLICATION NUMBER: US/09/620,312D
/ PRIOR FILING DATE: 2000-07-19
/ PRIOR APPLICATION NUMBER: 09/552,317

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; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_fl_genes Version 1.0
; SEQ ID NO: 8
; LENGTH: 1609
; TYPE: DNA
; ORGANISM: Homo sapiens.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (309)..(1202)
US-09-620-312D-8

Alignment Scores:
Pred. No.: 1,12e-96 Length: 1609
Score: 1392.00 Matches: 267
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 99.26% Mismatches: 0
Query Match: 46.02% Indels: 0
DB: 4 Gaps: 0

US-09-970-076-6 (1-564) x US-09-620-312D-8 (1-1609)
QY 1 MetAlaThrAlaGluArgArgAlaLeuGlyIleGlyPheGlnTrpLeuSerLeuAlaThr 20
DB 309 ATGGCCAGCGCGGAGCGAGAGCCCTCGGCATCGGCTTCCTCTTGGCCACT 368
QY 21 LeuValLeuIleCyAlaGlyGlnGlyArgArgGluAspGlyGlyProAlaCysTyr 40
DB 369 CTGGGCTCATCTGCGCGCGGAGCGGAGCGGAGAGATGGGGGTCTACCTGCTAC 428
QY 41 GlyGlyPheAspLeuTyrPheIleLeuAspGlySerGlySerValLeuHisIleTrpAsn 60
DB 429 GCGCGATTGACCTGACTTCACTTTTGCACAAATCAGGAAGTGTCTGCACACCTGAAAT 488
QY 61 GluIleTyrTyrPheValGluGlnLeuAlaHisIleValPheIleSerProGlnLeuArgMet 80
DB 489 GAAATCTATTACTTGTGGACAGTTGGCTCAAAATTCATCAGCCACAGTTGAGAAATG 548
QY 81 SerPheIleValPheSerThrArgGlyThrThrLeuMetIleValLeuThrGluAspArgGlu 100
DB 549 TCTCTTATTGTTTCTTCCACCGGAGAACACTTAAATGAACTGACAGAAACAGAGA 608
QY 101 GlnIleArgGlnGlyLeuGlnGluLeuGlnIleValLeuProGlyGlyAspThrTyrMet 120
DB 609 CAAATCCGTCAGAGGCTAGAGAACTCCAGAAAGTTCTGCCAGAGAGACACTTAACTAG 668
QY 121 HisGlnGlyPheGluArgAlaSerGlnGlnIleTyrTyrGluAsnArgGlnIleTyrArg 140
DB 669 CATGAAGGATTGAAAGGCGCAGTAGCAGATTATATGAAACAGACAGAGGATACAG 728
QY 141 ThrAlaSerValIleIleIleLeuThrAspGlyGluLeuHisIleAspLeuPhePheTyr 160
DB 729 ACAGCAGGCTCATCTTCTTGACTGATGAGAACTCCAGAGATCTCTTTTTCAT 788
QY 161 SerGluArgGluAlaAsnArgSerArgAspLeuGlyAlaIleValIleTyrCysValGlyVal 180
DB 789 TCAGAGAGGAGGAGCTAAATGATCTGAGATCTTGGGCAATGTTTACTGTTGTGTGG 848
QY 181 LysAspPheAsnGlnThrGlnLeuAlaArgIleAlaAspSerIleAspIleValPhePro 200
DB 849 AAAGATTTCATAGACACAGCTGGCCGATGGCGAGACAGTAAAGATCATGTGTTCC 908
QY 201 ValAsnAspGlyPheGlnAlaLeuGlnGlyIleIleIleSerIleLeuGlyIleSerCys 220
DB 909 GTGAATGACGGCTTTCAGGCTCTGCAAGGATCATCTCAATTTTGAAGAAGTCTCC 968
QY 221 IleGluIleLeuAlaAlaGluProSerThrIleCysAlaGlyGluSerPheGlnValVal 240
DB 969 ATCGAAATTTCTAGCAGCTAACCATCCACATATGTGCGAGAGATCATTTTAACTTGC 1028
QY 241 ValArgGlyAsnGlyPheArgHisAlaArgAsnValAspArgValLeuCysSerPheIle 260
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DB 1029 GTGAGAGAAACGGCTTCGACATGCCCGGACACGTGACAGGCTCTCTGACGTTCAAG 1088
QY 261 IleAsnAspSerValThrLeuAsnGlu 269
DB 1089 ATCAATGACTCGGTCCACACTCAGTAAAG 1115

RESULT 3
US-09-165-264-12/C
; Sequence 12, Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
; APPLICANT: Vinayagamorthy, Thuralayah
; TITLE OF INVENTION: Multi-Loci Genomic Analysis
; FILE REFERENCE: 44747
; CURRENT APPLICATION NUMBER: US/09/165,264
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 12
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-12

Alignment Scores:
Pred. No.: 4.04e-08 Length: 318
Score: 213.00 Matches: 36
Percent Similarity: 60.66% Conservative: 1
Best Local Similarity: 59.02% Mismatches: 24
Query Match: 7.04% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-6 (1-564) x US-09-165-264-12 (1-318)
QY 502 HisThrSerSerProProProAlaProIleTyrThrProProProProAlaProHisCys 521
DB 310 CACACACCAACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 251
QY 522 ProProProProProSerAlaProThrProProIleProSerProProSerThrLeuPro 541
DB 250 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 191
QY 542 ProProProGlnAlaProProProAsnArgAlaProProProSerArgProProProArg 561
DB 190 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 131
QY 562 Pro 562
DB 130 CCC 128

RESULT 4
US-09-165-264-14/C
; Sequence 14, Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
; APPLICANT: Vinayagamorthy, Thuralayah
; TITLE OF INVENTION: Multi-Loci Genomic Analysis
; FILE REFERENCE: 44747
; CURRENT APPLICATION NUMBER: US/09/165,264
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 14
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-14
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-618-166-209 SEQUENCE DESCRIPTION: SEQ ID NO: 209:

Alignment Scores:
Pred. No.: 0.000168 Length: 51259
Score: 205.50 Matches: 37
Percent Similarity: 70.18% Conservative: 3
Best Local Similarity: 64.91% Mismatches: 12
Query Match: 6.79% Indels: 5
DB: 4 Gaps: 2

US-09-970-076-6 (1-564) x US-09-618-166-209 (1-51259)
Qy 506 ProProProAlaProIleYrThrProProProProAlaProHiScySProProProPro
Db 46 CCGCCCTCAGCTCTGCTTTCAGCTCTGTCTCTCTCTCT-----CGCCCTCTCT 99

Qy 526 ProSerAlaProThrProProIleProSerProProSerThylLeuProProProGln
Db 100 CCGGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT-----CGCCCTCTCT 150

Qy 546 AlaProProProAsnArgLalProProProSerArgProProProArgPro 562
Db 151 GCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 201

RESULT 9
US-09-165-264-11/C
; Sequence 11, Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
; APPLICANT: Vinayagamoorthy, Thuraiyah
; TITLE OF INVENTION: Multi-Loci Genomic Analyses
; FILE REFERENCE: 44747
; CURRENT APPLICATION NUMBER: US/09/165,264
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-11

Alignment Scores:
Pred. No.: 1.65e-07 Length: 320
Score: 205.00 Matches: 35
Percent Similarity: 61.02% Conservative: 1
Best Local Similarity: 59.32% Mismatches: 23
Query Match: 6.78% Indels: 0
DB: 3 Gaps: 0

US-09-970-076-6 (1-564) x US-09-165-264-11 (1-320)
Qy 504 SerSerProProProAlaProIleYrThrProProProProAlaProHiScySProPro
Db 305 TCTGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 240

Qy 524 ProProProSerAlaProThrProProIleProSerProProSerThylLeuProProPro
Db 245 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 160

Qy 544 ProGlnAlaProProProAsnArgLalProProProSerArgProProProArgPro 562
Db 185 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 129

RESULT 10
US-09-165-264-8/C
; Sequence 8, Application US/09165264

```

Patent No. 6197510  
GENERAL INFORMATION:  
APPLICANT: Vinayagamoorthy, Thuralayah  
TITLE OF INVENTION: Multi-Loci Genomic Analysis  
FILE REFERENCE: 44747  
CURRENT APPLICATION NUMBER: US/09/165,264  
CURRENT FILING DATE: 1998-10-01  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 8  
LENGTH: 319  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: primer sequence  
US-09-165-264-8

Alignment Scores:  
Pred. No.: 2,33e-07 Length: 319  
Score: 203.00 Matches: 35  
Percent Similarity: 58.33% Conservative: 0  
Best Local Similarity: 58.33% Mismatches: 25  
Query Match: 6.71% Indels: 0  
DB: 3 Gaps: 0

US-09-970-076-6 (1-564) x US-09-165-264-8 (1-319)

Qy 503 ThisSerSerProProAlaProIleTyThrProProProProAlaProHisCyAPro 522  
Db 301 ACCC 242

Qy 523 ProProProSerAlaProThrProProIleProSerProProSerThrIleuProPro 542  
Db 241 CC 182

Qy 543 ProProGlnAlaProProProAsnArgAlaProProProSerArgProProProArgPro 562  
Db 181 CC 122

RESULT 11  
US-09-547-693-234  
Sequence 234, Application US/09547693  
Patent No. 6639050  
GENERAL INFORMATION:  
APPLICANT: Kieliszewski, Marcia  
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich  
FILE REFERENCE: OHU-04089  
CURRENT APPLICATION NUMBER: US/09/547,693  
CURRENT FILING DATE: 2000-04-12  
NUMBER OF SEQ ID NOS: 236  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 234  
LENGTH: 324  
TYPE: DNA  
ORGANISM: Artificial/Unknown  
FEATURE:  
NAME/KEY: misc.feature  
OTHER INFORMATION: Synthetic  
US-09-547-693-234

Alignment Scores:  
Pred. No.: 4.39e-07 Length: 324  
Score: 199.50 Matches: 43  
Percent Similarity: 54.26% Conservative: 8  
Best Local Similarity: 45.74% Mismatches: 38  
Query Match: 6.60% Indels: 5  
DB: 4 Gaps: 2

US-09-970-076-6 (1-564) x US-09-547-693-234 (1-324)

Qy 473 ProGlnProGlyASP-ThrGlyArgCysIleAsnProThrArgVallyeAsnAsnGlnPr 492  
|||||

Db 5 CTCACACCCGGGCGCTCCACACACACACCTTCACTCCACCCCGCATCTCCACACACACCTT 64  
Qy 492 oAlaIyTyProIleuAsnAsnAlaTyH:sthrSerSer-ProProProAlaProIleT 512  
Db 65 CACCTCCACCCCGATCTCCACACACACCTTCACTCCACCCCGCATCTCCACACCA---C 121

Qy 512 yThrProProProAlaProHisCyAProProProProProSerAlaProThrProP 532  
Db 122 CTCACCTCCACCCCGATCTCCACACACACCTTCACTCCACCCCGCATCTCCACACCA 181

Qy 532 roIleProSerProProSerThrIleuPro-----ProProGlnAlaProProProA 550  
Db 182 CTCACCTCCACCCCGATCTCCACACACACCTTCACTCCACCCCGCATCTCCACACCA 241

Qy 550 snArgAlaProProProSerArgProProProArgPro 562  
Db 242 CTCACCTCCACCCCGATCTCCACACACACCTTCACTTCACTT 279

RESULT 12  
US-08-658-136-1  
Sequence 1, Application US/08658136  
Patent No. 6071717  
GENERAL INFORMATION:  
APPLICANT: KLINGER, KATHERINE W  
APPLICANT: LANDES, GREGORY M  
APPLICANT: BURN, TIMOTHY C  
APPLICANT: CONNORS, TIMOTHY D  
APPLICANT: DACKOWSKI, WILLIAM  
APPLICANT: GERMINO, GREGORY  
APPLICANT: QIAN, FENG  
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENZYME CORPORATION  
STREET: ONE MOUNTAIN ROAD  
CITY: FRAMINGHAM  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 01701

COMPUTER READABLE FORM.  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/658,136  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: LASSEN, ELIZABETH  
REGISTRATION NUMBER: 31,845  
REFERENCE/DOCKET NUMBER: GEN4-17.8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 508-872-8400  
TELEFAX: 508-872-5415  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 53577 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-658-136-1

Alignment Scores:  
Pred. No.: 0.000556 Length: 53577  
Score: 199.00 Matches: 91  
Percent Similarity: 32.35% Conservative: 29  
Best Local Similarity: 24.53% Mismatches: 124  
Query Match: 6.58% Indels: 128  
DB: 3 Gaps: 16

US-09-970-076-6 (1-564) x US-08-658-136-1 (1-53577)



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Oy      555 ---ProSerArgProProPoaAsgProSerVal 564
Db      34680 CTCCTCCTCCCTCCTCCTCCCTCCCTCCCTCCTT 34712
...:

RESULT 13
US-08-781-891-208
Sequence 208, Application US/08781891
Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-Bn
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
City: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620Leunburg Ph. D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 16442 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-781-891-208

Alignment Scores:
Pred. No.:          0.00219           Length:       16442
Score:              195.00            Matches:        36
Percent Similarity: 61.90%            Conservative:   3
Best Local Similarity: 57.14%         Mismatches:    22
Query Match:        6.45%             Indels:         2
DB:                  3                Gaps:           1
US-09-970-076-6 (1-564) x US-08-781-891-208 (1-16442)
Oy      503 ThisSerSerProProProlaAProIleYrThrProProProProlaAProHtCySPro 522
Db      16183 TCCTTCCTCTCTCTCTTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 16242
Oy      523 ProProProProSerAlaProThrProProIleProSerProProSerThrIeuProPro 542
Db      16243 CTCCTCGCTCTCTCTGCTCTCTCTCTCTCTCTGTGCTCTGCTCTCTCTCTCTCTCTCT 16302
Oy      543 Pro-----ProGlnAlaProProProProlaAArgAlaProProProSerArgProPro 560
Db      16303 CTCCTCGCTCTCTCTCTCTCTCTCTCTCTCTCGCTCTCGCTCTCTCTCTCTCTCTCT 16362
Oy      561 ArgProSer 563
Db      16363 GCCTCTGCT 16371

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Db 33956 GGTAAGATGCCCCACCTGCTAC-----CTGCCCGCATGCTGCCAG 34000  
Qy 360 uGluSerGluGluGluAspAspAspGlyLeuProGlyLysTrpProThrValAspAl 380  
Db 34001 GGCACTGGGTTGAGCCCCAGGGC-----AGACGGGACGCTGGCCAGAGACTGAGC 34054  
Qy 380 aSerTrpTrpGly----- 384  
Db 34055 CTCAGACCTGGCTCTCTCTCCATGAGGTTCTCGGTCTGACCTGCTTCAATAGCC 34114  
Qy 385 -----GlyArgGlyValGlyLysLeuAsp 393  
Db 34115 TCAGCCGTTCTGCTCTGTGTAAAGAGAGTGTCTTGGGGAGCCAGGAGGTAAAGAG 34174  
Qy 393 gMetGluValArgTrpGlyGlyLysLeuSerThrGluGluGlyAlaLysLeuGluLysAl 413  
Db 34175 G-----GCCCAAGTGT-GGGAGAGGACTAAGAGATG 34206  
Qy 413 ALyAsnAlaArgValLysMetProGluGluGluTrpGluPheProGluProArgAsnLe 433  
Db 34207 CTGCTGTGCTGCTCCACTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT----- 34258  
Qy 433 uAsnAsnAsnMetArgArgProSerSerProArgLysTrpTrpLysProLysGlyLys 453  
Db 34259 -----AGCCCTCCCTCTCT-----CCCTCCCTCCAGCC 34287  
Qy 453 sLeuAspAlaLeuTrpValLeuLeuArgLysGlyTyraAspArgValSerValMetArgPr 473  
Db 34288 CTTCCTCTCTCTCCCTCCCTCTA-----GCCCTTCTCTCTTCCCTCC 34329  
Qy 473 oGlnProGlyAspThrGlyArgCysAlaAsnPheThrArgValLysAsnAsnGlnProAl 493  
Db 34330 CCAGCCCTCTCCCTCTCTCCCTCCCTGACCTTCCCTCTCCCTCCCTCCCTCCCTTC 34389  
Qy 493 aLysTrpProLeuAsnAsnAlaTy-----HisThrse 504  
Db 34390 CCTCTCTCTCTCCCTGACCTTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTGC 34449  
Qy 504 r-----SerPr 506  
Db 34450 CCCCAGCCCTCTCCCTCCCTGACCTTCCCTCCCTCTCTCCCTCTCCCTCCCTCCCTCC 34509  
Qy 506 oProProAlaProIleTyThrProProPro-----ProAl 518  
Db 34510 TCCTCCCTCTCTCTCTCTCTCCCTCCCTCTCTCCCTCTCTCCCTCTCTCCCTCCCT 34569  
Qy 518 aProHisCysProPro-----ProProProSerAlaProThrProProIleProSerPr 536  
Db 34570 CCCCTCC 34629  
Qy 536 oProSerThrLeuProProProProProGlnAlaProProProAsnArgAlaProPro----- 554  
Db 34630 CT 34683  
Qy 555 ----ProSerArgProProProProArgProSerVal 564  
Db 34684 CCTCCCT 34717

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